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MOAT-B
MRP 1 MALRGFCSADGSDPLWDMVNTWNTSNPDFTKCFONTVLVWPCFYWACFPFYFLYLSRHRDGYIOMTPLNKTXTALGFLWIVCHADLFYSFWERSGI 100

MOAT-B 1MLP 3

MRP 101 FLAPVFLVSPITLLGITTLLATFLIOLERRKGVQSSGIMLTFWLVALCALILRSKINTALKEDAQVDLFRDITFYVYFSLLLIQLVLSCFSDRSPLFSE 200

MOAT-B 4 VYQEVKPNPLQDANICSRVFFWMLNPLFKIGHKRRLEEDDHYSVLPEDRSQHLGEELQGFWDKEVLRAENDAOK 77

MRP 201 TIHDPNPCPESSASFLSRITFWMITGLIVRGYRQPLEGSDLSLNKEDTSEQVVPVLVKNWKKCAKTRKOPVKVYSSKDPAPQKSSKVDANEVEAL 300

MOAT-B 78PSLTRAIIKCYWKSVLVLGIFTLIEESAKVIQPIFLGKIINVFENYDPHDSVALNTAYAYATVLTFTLILAILHHLYFYHVQACAGMRL 166

MRP 301 IVKSPQKEWNPFLFKVLYKTGPGYFLMSFFFAIHDLMHFGSGPQILKLLIKFVNDTKAPDWQGYFYTLLFVTACQLTLVLHQYFHCIFVSGHRI 395

MOAT-B 167 RVAMCHMIYRKALRLSNMAGKTTTGCQIVNLLSNDVNKFDVTVFLHFLWAGPLQAIATALLWMEIGISCLAGHAVLIIILLPLQSCFCGLFSSLSRKTA 266

MRP 396 KTAIVGAVYRKALVITNSARKSSVTGEIVNLHMSVDAQRFMDLATYINMIWSAPLOVILALYLLWNLGPSVLAVGVVLMVPMNAVMAHMTKTYQVAHM 495

MOAT-B 267 TFTDARIRTHNEVITGIRIIXMYAWEKSFSNLITNLRKKEISKILRSSCLRGHNLASFFSASKIIVFVTFTTYVLLG...SVITASRVFVAVTLYGAVRLT 364

MRP 496 KSKDNRIKLMNEILNGIKVLKLYAWELAFKDKVLAIHQEELKVLKSAYLSAVGTFTWCTPFLVALCTFAVYVITIDENILDAQTAFVSLALFNILRFP 595

MOAT-B 365 VTLFFPSAIERVSEAIVSIRRIOTFLLLDEIS...ORNRLPSDGKKMHVQDPTAFWDKASETPTLQGLSFTVRPCELLAVVGPVGACKSSLLSAVLG 460

MRP 596 LNI.LPMVISSIVQASVSLKRLRIFLSHEELEPDSIERRPVKGGGTNSITVRNATFTWAR.SDPPTLNGITFSIPEGALVAVVGQVCGCKLSLLSALLA 693

MOAT-B 461 ELAPSHGLVSVHGRIAYVSQPPWVFSCTLRNSNIFGKKYKERYEKVIKACALKKDLQLLEDGDLTVIGDRGTTLSGGQKARVNLARAVYQDADIYLLDD 560

MRP 694 EMDKVEGHVAIKGSVAYVPOQAWIQNDSIRENIFGQCLEEPPYRSVIOACALLPDLILPSGDRTEIGEGVNLSCGQKQVSLARAVYSNADIYLFDD 793

MOAT-B 561 PLSAVDAEVSRLHFLCICO...ILHEKITLVTHQLQYLKAASQILILKDGKMHVQKGTYTEFLKSGIDFGSLK...KDNEESEOPPVPV... 645

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MOAT-B 646TPTLRNRTFSESSVWSQSSRPSLKDGALESQDT...ENVPTLSEENRSEKGVGFOAYKMYFACAHWIVFIFLILLNTAAQVAVYVLO 731

MRP 894 KQENGMLVTDGACKQLQRLSSSSSYSGDISRHHNSTAELQKAEAKKEETWKLHEADKAQTQVQLSVYWDYKKAIGLIFISFLSIFL.MCNHVSALAS 992

MOAT-B 732 DWLWLYWANKQSHLNVTVNGGNTVEKLDLWLYLGIYSGLTATVTLFGIARSLLVFVVLVNSQTLHNKMFESILKAPVLFDRNPGRILNRFSKDIGH 831

MRP 993 NYWLSLWTD...DPIVNGTQHTKVR...LSVYGALGISQGIADVGYSHAVSIGGILASRCLHVDLLHSILRSPHSFFERTPSGNLVNRFSEKELDT 1082

MOAT-B 832 LDDLLPLTFLDFIQTLQVVGVSVAIVIPWIAIPLVPLGIIIFILRRYFLETSSRDVRLSTTRSPVFSHLSSSLOGLWITRAYKAERCOELFDAHQ 931

MRP 1083 VDSHIEVIMKFMGSLFNVIGACIVILLATPIAAIIIPPLGLIYFFVQRFYVASSRQLKRESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLV 1182

MOAT-B 932 DLHSEAWFLFTLTSRWFVRLDAICAMPVIIIVAFGSLILAKTLDAQVGLALSVALTLHGMFOWCVROSAEVENMMISVERVIEYTDLEKEAPWEYOK.R 1030

MRP 1183 DENOKAYYPSIVANRWLAVRLECVGNCIVLFAALFAVISRHLSAGLVGLSVSYLQVTTYNLWLVMSSEMETNIVAVERLKEYSETEKEAPWQIQETR 1282

MOAT-B 1031 PPPAWPHEGVIIIDNVNFMYSPPGGLVLKHLTALIKSOEKVGIVGRGTAGKSSSLSALFRLSE.PEGKIWDKILTTEIGLHDLRKKHSIIPQEPVLFTG 1129

MRP 1283 PPSWPPQVGRVEFRNYCLRYREDLDFVLRHINVTINGGEKVGIVGRGTAGKSSLTGLFRINESAECEIIGDINIAGIHLHDLRFKITIIPQDPVLFSG 1382

MOAT-B 1130 THRKNLDPFKENTDEELWALQEVOLKETIEDLPKMDTELAESGSNFSVGQRLVCLARAILRKNQILIIDATANVDPRTDELIOKKIREKFAHCTVL 1229

MRP 1383 SLRNHLDPFSQYSDVEEVTSLSLAHLKDFVSALPDKLDHECAEGENLSVGQRLVCLARALLRKTILVLEATAVDETDLLIQSTIRTQFEDCTVL 1482

MOAT-B 1230 TIAHRLNTIIDSCKIMVLDSGRLEKEYDEPYVLLONKESLFYKMWQQLKAEAAALTETAKQVYFKRNYHIGHTDHMTNTSNGOPSTLTIFETAL 1325

MRP 1483 TIAHRLNTIMDYTRIVLDKGEIQEYGA PSDLLOOR.GLFYSMAKDAGLV 1531

Figure 1

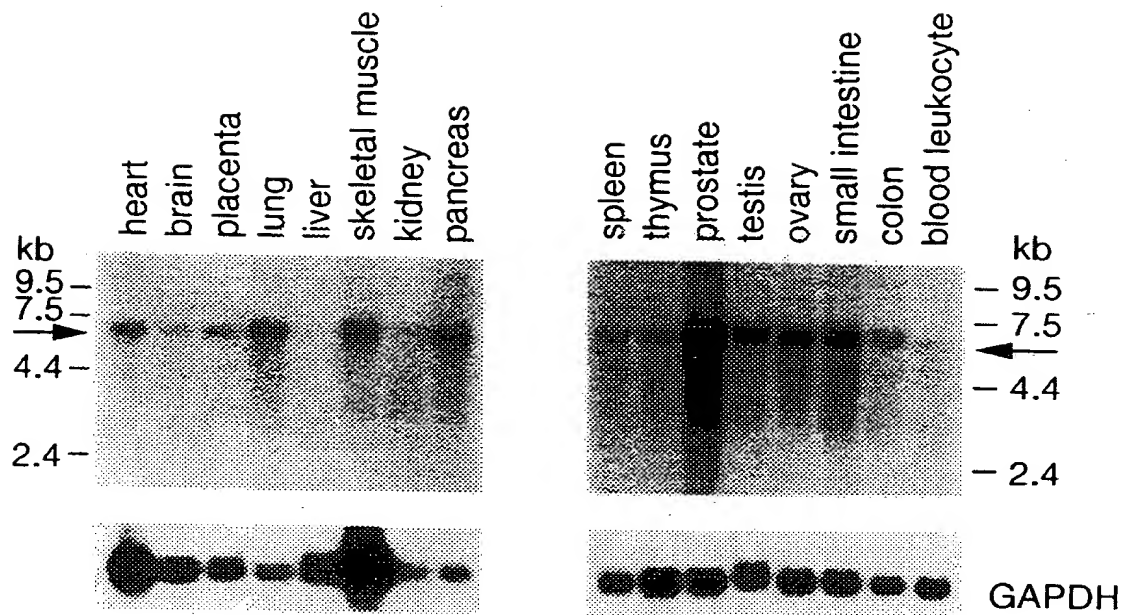


Figure 3

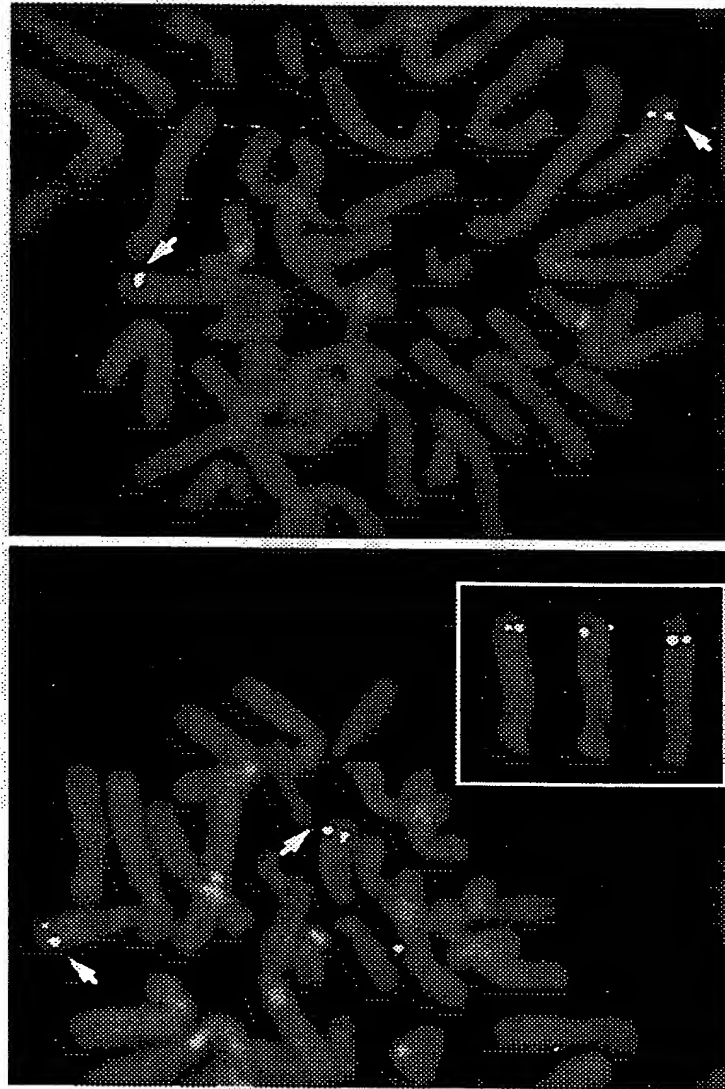


Figure 4

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Fig. 5A

1 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRR TRPLECQDAL ETAARAEGLS
 61 LDASMHSQLR ILDEEHPK GK YHHGLSALKP IRTTSKHQHP VDNAGLFSM TFSWLSSLAR
 121 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTL
 181 TM1 LSIVCLMITQ LAGFSGPAPM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW TM2
 241 TM3 ALNYRTGVRL RGAILTMAFK KILKLNKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG
 301 TM4 PVVAILGMIY NVIILGPTGF LGSVAVFILFY PAMMFASRLT AYFRKCVAA TDERVQKMNE
 361 TM5 VLTYIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV
 421 TM6 HMTLGFDLTA AQFTVVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK
 481 NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPEMKKDK RASRGKKEKV RQLQRTEHQA
 541 NBF1 VLAEQKGHL LDSERPSPE EEEGKHILG HLRLQRTLS IDLEIQEGKL VGICGSVSGG
 601 A KSLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS
 661 CCLRPDLAIL PSSDLTEIGE RGANLSGGQR ORISLARALY SDRSIYILDD PLSALDAHV
 721 NBF1 B NHIFNSAIRK HLKSKTVLFV THQLQYLVDC DEVIFMKEGC ITERGTHEEL MNLNGDYATI
 781 FNNLLGETP PVEINSKKEG SGQKKSQDK GPKTGSVKKE KAVKPEEQOL VOLEEKQOGS
 841 TM7 VPWSVYGVYI QAAGGPLAF L VIMALFHLNV GSTAFSTWWL SYWIKQSGN TTVTRGNETS
 901 TM8 VSDSMKDNPH MQYYASIIAL SMAVMLILKA IRGVVFKGT LRASSRLHDE LFRRILRSPM
 961 TM9 KFFDTTPTGR ILNRFSKMD EVDVRLPFA EMFIONVILV FFCVGMIAV FPWFLVAVGP
 1021 TM10 LVILFVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG OEFLHRYQEL
 1081 TM11 LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISTAVOLT
 1141 TM12 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM
 1201 NBF2 RYRENPLVL KKSFTIKPK EKIGIVGRTG SGKSSLGMA FRLVELSGGC IKIDGVRISD
 1261 IGLADLRSL SIIPQEPVLF SGTVRNLD PNOYTEDQIW DALERTHME CIAQLPLKLE
 1321 SEVMENGDNF SVGEROLL CI ARALLRECKI LILDEATAAM DTETDLLIQE TIREAFADCT
 1381 C B MLTIAHRLHT VLGS DRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG

Fig. 5B

1 MGPMDALCGS GELGSKFWDS NLSVHTENPD LTPCFQNSLL AWVPCIYLVW ALPCYLLYLK TM1
 61 HHCRGYIILS HLSKLMVLG VLLWCVSWAD LFYSFHGLVH GRAPAPVFFV TPLVVGVTML TM2
 121 LATLLIQYER LQGVSSGVL IIFWFLCVVC AIVPFRSKIL LAKAEGEISD PFRFTTFYIH TM3
 181 FALVLSALIL ACFREKPPFF SAKNVDPNPY PETSUGFLSR LFFWWFTKMA IYGYRHPLEE TM4
 241 KDLWSLKEED RSQMVVQQLL EAWRKQEKQT ARHKASAAPG KNASGEDEV L LGARPRPRKP TM5
 301 SFLKALLATF GSSFLISACF KLIQDILLSFI NPQLLSILIR FISNPMAPSW WGFLVAGLMF TM6
 361 LCSMMQSLIL QHYHYIYFVT GVKFRTGIMG VIYRKALVIT NSVKRASTVG EIVNLMVSVA TM7
 421 QRFMDLAPFL NLLWSAPLOI ILAIYFLWQN LGPSVLAGVA FMVLLIPLNG AVAVKMAFQ TM8
 481 VKQMKLDSR IKLMSEILNG IKVLKLYAWE PSFLKQVEGI RQGEQLLRT AAYLHTTTTF TM9
 541 TWMCSPLVLT LITLWVYVYV DPNNVLD AEFVSVSLFNI LRLPLNMLPQ LISNLTQASV TM10
 601 SLKRIQQFLS QEELDPOSVE RKTISPGYAI TIESGTFTWA QDLPTTLHSL DIQVPKGALY TM11
 661 AVVGPVCGCK SSLVSALLGE MEKLEGKVHM KGSVAIVPQO AWIONCTLOE NVLFGKALNP NBF1
 721 KRYQOTLEAC ALLADLEMLP GGDQTEIGEK GINLSGGORQ RVSLARAVYS DADIFLLDDP A
 781 LSAVDSEVAK HIFDEVIGPE GVLAKTRVL VTHGISFLPQ TDFIIVLADG QVSEMGYPYA NBF1
 841 LLQRNGSFAN FLCNYAPDED QGHLEDSWTA LEGAEDKEAL LIEDTLSNHT DLTDNDPVTY C
 901 VVQKQFMRQL SALSSDGEQ GRPVPRRLG PSEKVQVTEA KADGALTQEE KAAIGTVELS B
 961 VFWDYAKAVG LCTTLAICLL YVGOSAAAIG ANVWLSAWTN DAMADSRQNN TSLRLGVYAA TM12
 1021 LGILQGFVLH LAAMAHAGG IQAARVLEQA LLENKIRSPQ SFFDTTPSGR ILNCFSKDIY TM13
 1081 VVDEV LAPVI LMLLNSFFNA ISTLVVIMAS TPLFTTVILP LAVLYTLVQR FYAATSRQLK TM14
 1141 RLESVSRSPI YSHFSETVTG ASVIRAYNRS RDEFIISDTK VDAQORSCYP YIISNRWLSI TM15
 1201 GVEFVGNCVV LFAALFAVIG RSSLNPLGVG LSVSYSLQVT FALNWHIRM SDLESNIVAV TM16
 1261 ERVKEYSKTE TEAPWVVEGS RPPEGWPPRG EVEFRNYSVR YRPGDLVLRL DLSLEHVHGE TM17
 1321 KVGIVGRTGA GKSSMTLCLE RILEAAKGEI RIDGLNVADI GLHDLRSOLT IIPQDPILFS NBF2
 1381 GTLRHNLDPF GSYSEEDIWW ALELSHLHTF VSSQAGLDF QCSEGGENLS VGQRQLVCLA A
 1441 RALLRKSRL VLDEATAAID LETDNLIQAT IRTQFDTCTV LTIAHRLNTI MDYTRVLVLD NBF2
 1501 KGVVAEFDSP ANLIAARGIF YGMARDAGLA B

Nucleotide Binding Fold I

MOAT-B	HSLDITQVPK	CAVAVVGVFV	UGCKR99VLS	LAENKLEK	HM	KFSVAVV	ATG	CCCLCE	704	
MRP	NGCTFSSEPE	CAVAVVGVFV	LAENKQVSG	HA	AI	KFSVAVV	ATG	CCCLCE	727	
MOAT-C	VRQNVNLDMA	CAVAVVGVFV	BSKSSLSA	MUGSENVII	HI	AI	CTTAVV	ATG	CCCLCE	717
MOAT-C	HSLDLDEGE	CAVAVVGVFV	BSKSSLSA	ICGLILG	ST	TI	CTTAVV	ATG	CCCLCE	717
MOAT-B	ICGLSTFTVRP	CAVAVVGVFV	BSKSSLSA	VGLCLAPSHS	AI	STFTAVV	ATG	CCCLCE	717	
CFTR	KIDNFKBER	COLLAFAST	CAVAVVGVFV	ITLLEPS	KI	SV	HRIIVAVV	PMVFGSL	LRS	491
SUR	ENGLNITPE	CGNTNGLNS	UGCKR99VLS	LAENKQVSG	AI	FWSVSDG	EIGEDSPSP	ETATOLDIRK	RPLVAVV	785
MDR1	KGNIANKVQS	CGNTNGLNS	UGCKR99VLS	MORLYDPT	MSVSDGDPT	TINVRFLREI	IGVGEV	PVLVAT	786	

MOAT-D	MLNLFCA.LN	PKAYFTLEA	CALLADCEEM	EGCGEIGE	KINLGGGR	QFVGLARAV	SADDFLLDD	PUSVALSYA	KHIDHV	793
MRP	NILTFCCO.LE	GYFYSRFLQ	CALLDCEIE	EGCGEIGE	KINLGGGR	QFVGLARAV	SINDFLLDD	PLSADVHSA	KHIDHV	790
cMOAT	NILTFCKE.FN	KEFNVOCLLE	CALLDCEIE	EGCGEIGE	KINLGGGR	QFVGLARAV	QNLDFLLDD	PLSADVHSA	KHIDHV	803
MOAT-C	NILTFCKE.YD	KEFNVOCLNS	CALLDCEIE	EGCGEIGE	KINLGGGR	QFVGLARAV	SRSIVLLDD	PLSADVHSA	KHIDHV	727
MOAT-B	NILTFCKK.YE	KEFEKVKLE	CALLKDKQL	EDLDFLLVD	GTHLGGGR	QFVGLARAV	QADDFLLDD	PLSADVHSA	KHIDHV	577
CFTR	NILTFCKK.YE	KEFEKVKLE	CALLKDKQL	EDLDFLLVD	GTHLGGGR	QFVGLARAV	KADDFLLDD	PGYLVLTLE	KHIDHV	590
SUR	NILTFESP.FN	KCKMCKKLE	CALLDCEIE	EGCGEIGE	KINLGGGR	QFVGLARAV	QADDFLLDD	PLSADVHSA	KHIDHV	573
MDR1	RYRYRBNVT	MDIEKAVKE	ANAYDFTMK	EHKDFLLVD	QACGGGR	QFVGLARAV	RNPKFLLE	ATLALTESE	AVVQAL	871

Nucleotide Binding Fold II

MOAT-D	KADL	LHHVG	GEKVGV	WGRV	SACKSS	ITLC	EF	FL	LAAG	EPRG	GS	LWVR	DGLNLDL	ISQ	AI	TIPOB	I	FSGI	GLW	DPG	SGV	1392		
KRI	RHNVT	RG	AGKGV	WGRV	SACKSS	ITLC	EF	FL	LAAG	EF	SG	LR	SG	LDL	ISQ	AI	TIPOB	I	FSGI	GLW	DPG	SGV	1396	
MOAT	RGITC	CG	S	1	WGRV	SACKSS	ITNC	EF	FL	LAAG	CG	1	GV	DL	ISQ	AI	TIPOB	I	FSGI	GLW	DPG	SGV	1403	
MOAT-C	KK	FT	AP	K	1	WGRV	SACKSS	ITNC	EF	FL	LAAG	CG	1	GV	DL	ISQ	AI	TIPOB	I	FSGI	GLW	DPG	SGV	1403
MOAT-B	KKLAL	TAL	KS	CG	GV	WGRV	SACKSS	ITNC	EF	FL	LAAG	CG	1	GV	DL	ISQ	AI	TIPOB	I	FSGI	GLW	DPG	SGV	1403
SUR	KHVNAL	SP	CG	1	WGRV	SACKSS	ITNC	EF	FL	LAAG	CG	1	GV	DL	ISQ	AI	TIPOB	I	FSGI	GLW	DPG	SGV	1403	
CFTR	INL	EF	SP	CG	1	WGRV	SACKSS	ITNC	EF	FL	LAAG	CG	1	GV	DL	ISQ	AI	TIPOB	I	FSGI	GLW	DPG	SGV	1403
MDR1	QGLLE	VEVKK	CG	1	WGRV	SACKSS	ITNC	EF	FL	LAAG	CG	1	GV	DL	ISQ	AI	TIPOB	I	FSGI	GLW	DPG	SGV	1403	

[illegible]

Fig. 6A

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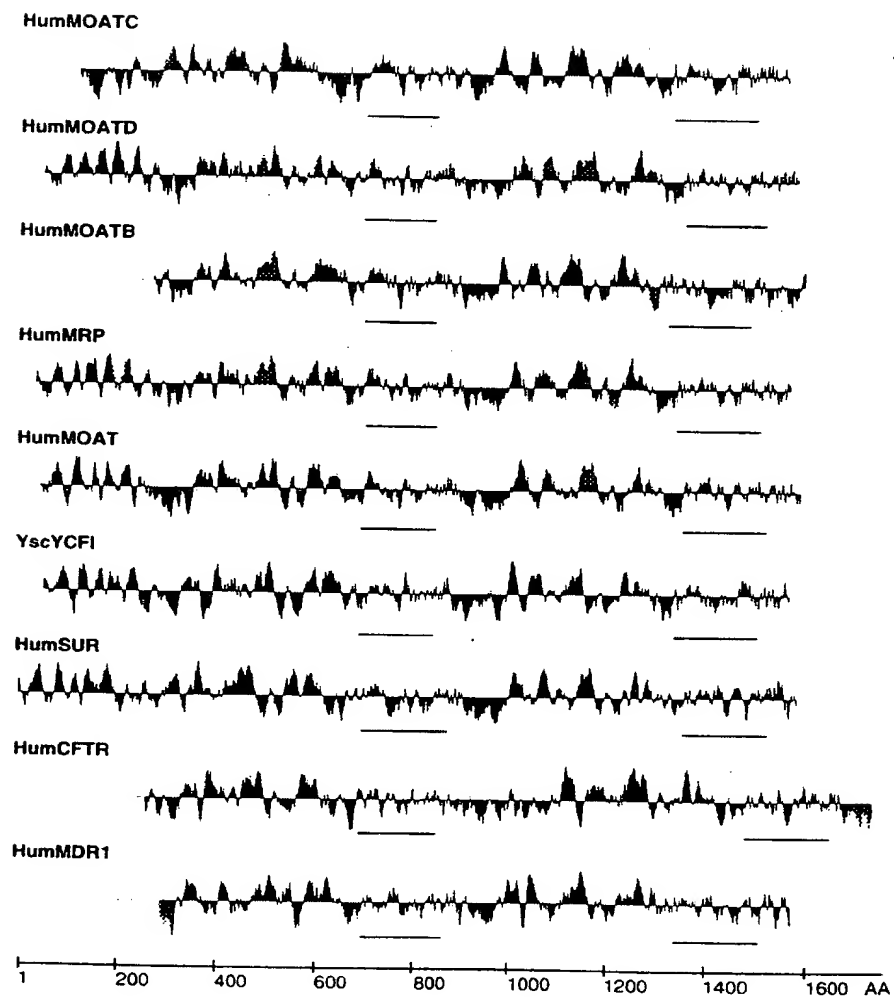


Fig. 6B

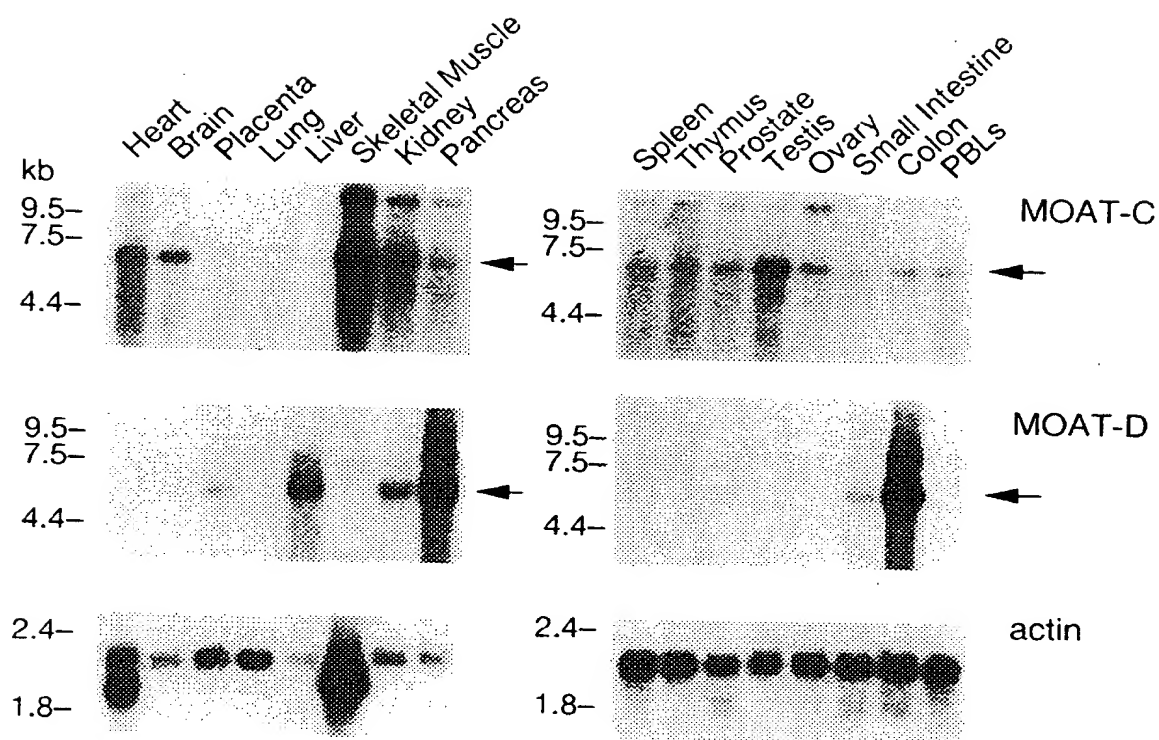
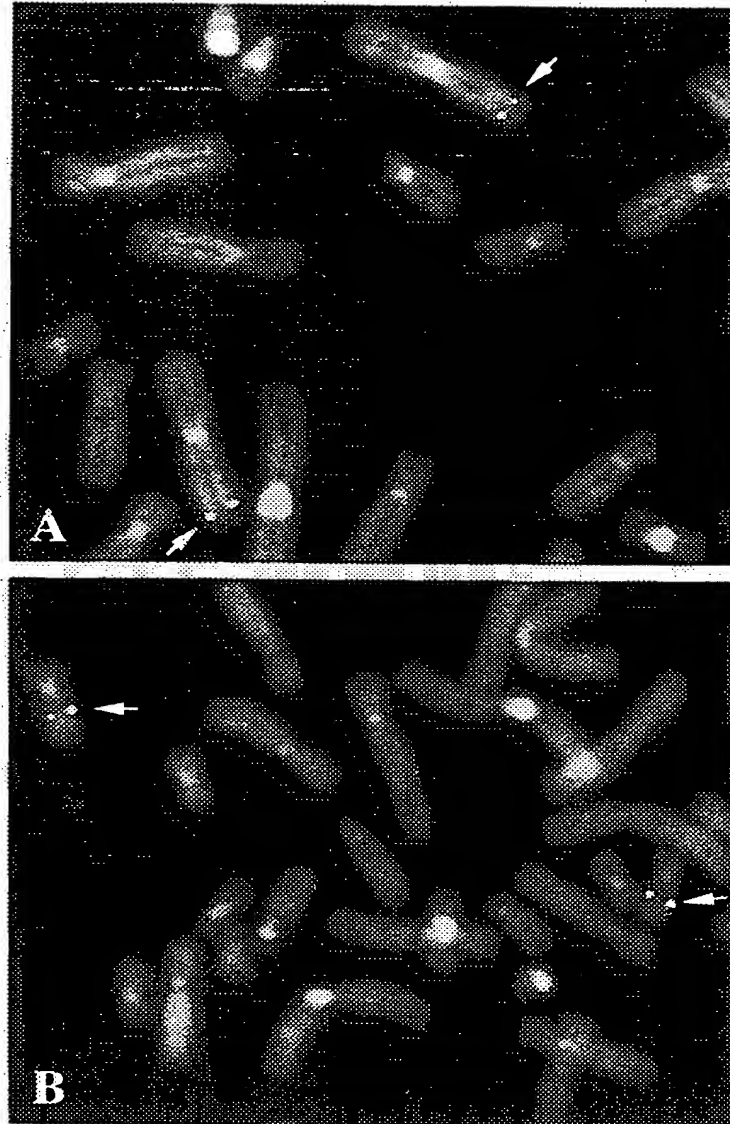


Figure 7

**Figure 8**

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1 MAAPAEPCAG QGVW[•]QTEPE PAATSLLSLC FLRTAGVWVP PHYLWVLGPI YLLFIHHHGR
 61 GYLRMSPLFK AKMVLGFALI VLCTSSVAVA L^WKIQOQTPE APEFLIHPTV WLT^TMSFAVF
 121 LIHTERKKGV OSSGVLFGYW LLCFVLPATN AAQOASGAGF QSDPVRHLST YLCLSLVVAQ
 181 FVLSCLADQP PFFPEDPQOS NPCPETGAAF PSKATFWWVS GLVWRGYRRP LRPKDLWSLG
 241 RENSSEELVS RLEKEWMRNR SAARRHNKAI AFKRKGGSGM KAPETEPFLR QEGSQWRPLL
 301 KAIWQVFHST FLLGTLSLII SDVFRPTVPK LLSLFLEFIG DPKPPANKGY LLAVLMFLSA
 361 CLQTLPEQQN MYRLKVPQMR LRS^AITGLVY RKVLALSSGS RKASAVGDV VNLVSDVQRL
 421 TESVLYLNGL WLPLVWIVVC FVYLWQLLGP SALTAIAVFL SLLPLNFFIS KKR^{NH}HQEEQ
 481 MRQKDSRRL TSSILRNSKT IKPHGWEGAF LDRVLGIRGQ ELGALRTSGL LFSVSLVSFO
 541 VSTFLVALV FAVHTLVAEN AMNAEKAFVT LTVLNILNKA QAFLPFSIHS LVQARVSFDR
 601 LVTFLCLEEV DPGVVDSSSS GSAAGKDCIT IHSATFAWSQ ESPPCLHRIN LTVPOGCLLA
 661 VVGPVGAGKS SLLSALLGEL SKVEGFVSIE GAVAYVPQEA WVQNTSVVEN VCFGQELDPP
 721 WLERVLEACA LQPDVDSFPE GIHTSIGEQG MNLSGGQKOR LSLARAVYRK AAVYLLDDPL
 781 AALDAHVGQH VFNQVIGPGG LLQGTTRILV THALHILPOA DWIIVLANGA IAEMGSYQEL
 841 LQRKGALVCL LDQARQPGDR GEGETEPGTS TKDPRGTSAG RRP^{EL}RRERS IKSVP^EKDRT
 901 TSEAQTEVPL DDPDRAGWPA GKDSIQYGRV KATVHLAYLR AVGTPLCLYA LFLFLCQOVA
 961 SFCRGYWLSL WADDPVAGGQ QTQAALRGGI FGLLGCLQAI GLFASMAAVL LGGARASRL
 1021 FORLLWDVVR SPISFFERTP IGHLLNRFSK ETD^TVDVDIP DKLRSLMYA FGLLEVSLV
 1081 AVATPLATVA ILPLFLLYAG FQSLYVSSC QLRRLESASY SSVCSHMAET FOGSTVVRAF
 1141 RTOAPFVAQN NARVDESQRI SFPRLVADRW LAANVELLGN GLVF^AAATCA VLSKAHLSAG
 1201 LVGFSVSAAL QVTQALQWV RNWTDLENSI VSVERMODYA WTPKEAPWRL PTCAAOPPPW
 1261 QGGQIEFRDF GLRYRPELPL AVQGVSLKIH AGEKVGIVGR TGAGKSLAS GLLRLQEAEE
 1321 GGIWIDGVPI AHVGLHTLRS RISIIPQDPI LFPGLRMNL DLLQEHSDEA IWA^ALETVQL
 1381 KALVASLPGQ LOYKCADRGE DLS^VVGQKQLL CLARALLRKT QILILDEATA AVDPGTELOM
 1441 QAMLGSWFAQ CTVLLIAHRL RSVMDCARVL VMDKGQVAES GSPAQLLAQK GLFYRLAQES
 1501 GLV

Figure 9

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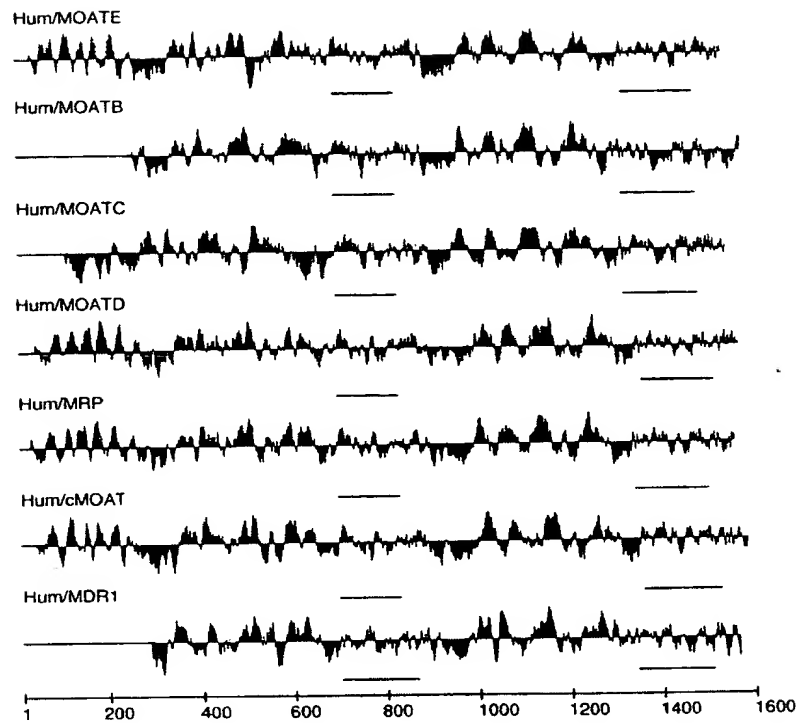


Figure 10

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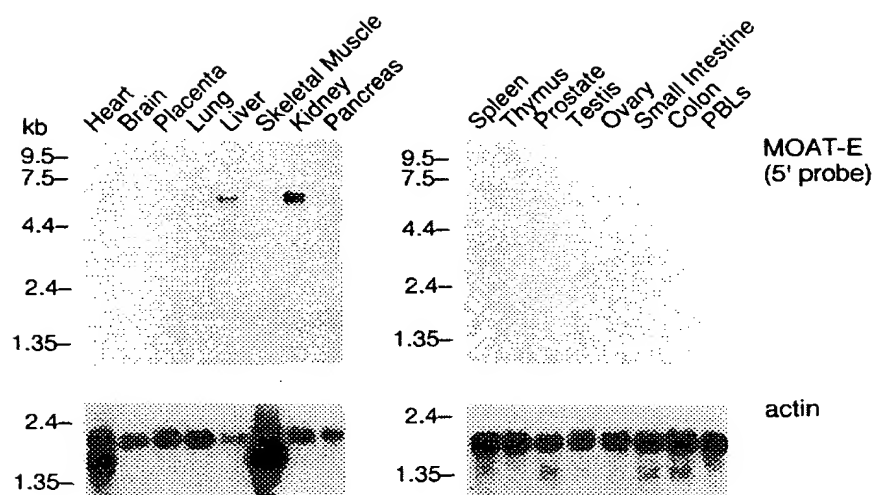


Figure 11

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PCT/US99/06644

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361 -----+-----+-----+-----+-----+ 420
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a E N Y D P M D S V A L N T A Y A Y A T V -

CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTATCACGTTTCTAG
 421 -----+-----+-----+-----+-----+ 480
 GACTGAAAAACGTGCGAGTAAAACCGATATGACGTAGTGAATATAAAAAATAGTGCAAGTC

a L T F C T L I L A I L H H L Y F Y H V Q -

TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT
 481 -----+-----+-----+-----+-----+ 540
 ACACGACCCTACTCCAATGCTCATCGGTACACGGTATACTAAATAGCCTTCCGTGAAGCA

a C A G M R L R V A M C H M I Y R K A L R -

CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT
 541 -----+-----+-----+-----+-----+ 600
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a L S N M A M G K T T T G Q I V N L L S N -

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 601 -----+-----+-----+-----+-----+ 660
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a D V N K F D Q V T V F L H F L W A G P L -

CAGGCGATCGCAGTGAAGTGCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG
 661 -----+-----+-----+-----+-----+ 720
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a Q A I A V T A L L W M E I G I S C L A G -

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 721 -----+-----+-----+-----+-----+ 780
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a M A V L I I L L P L Q S C F G K L F S S -

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 781 -----+-----+-----+-----+-----+ 840

Figure 12B

SUBSTITUTE SHEET (RULE 26)

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 a L R S K T A T F T D A R I R T M N E V I -
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 841 ----- + ----- + ----- + ----- + ----- + 900
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 a T G I R I I K M Y A W E K S F S N L I T -
 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT
 901 ----- + ----- + ----- + ----- + ----- + 960
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 a N L R K K E I S K I L R S S C L R G M N -
 TTGGCTTCGTTTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTGACCTTCACCACCTACGTG
 961 ----- + ----- + ----- + ----- + ----- + 1020
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 a L A S F F S A S K I I V F V T F T T Y V -
 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTTCGTTGGCAGTGACGCTGTATGGGGCT
 1021 ----- + ----- + ----- + ----- + ----- + 1080
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 a L L G S V I T A S R V F V A V T L Y G A -
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 1081 ----- + ----- + ----- + ----- + ----- + 1140
 CACGCCGACTGCCAATGGGAGAAGAAGGGGAGTCGGTAACTCTCCCACAGTCTCCGTTAG
 a V R L T V T L F F P S A I E R V S E A I -
 GTCAGCATCCGAAGAATCCAGACCTTTTGTCTACTTGATGAGATATCACAGCGCAACCGT
 1141 ----- + ----- + ----- + ----- + ----- + 1200
 CAGTCGTAGGCTTCTTAGGTCTGGAAAAACGATGAACTACTCTATAGTGTGCGGTTGGCA
 a V S I R R I O T F L L L D E I S O R N R -
 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT
 1201 ----- + ----- + ----- + ----- + ----- + 1260
 GTCGACGGCAGTCTACCATTTTCTACCACGTACACGTCCTAAAATGACGAAAAACCCTA

Figure 12C

WO 99/49735

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a Q L P S D G K K M V H V Q D F T A F W D .
AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCTTTACTGTCAGACCTGGCGAATTG
1261 ----- + ----- + ----- + ----- + ----- + ----- + 1320
TTCCGTAGTCTCTGGGGTTGAGATGTTCCGGAAAGGAAATGACAGTCTGGACCGCTTAAC

a K A S E T P T L Q G L S F T V R P G E L .
TTAGCTGTGGTTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG
1321 ----- + ----- + ----- + ----- + ----- + ----- + 1380
AATCGACACCAGCCGGGGCACCCTCGTCCCTTCAGTAGTGACAATTCACGGCACGAGCCC

a L A V V G P V G A G K S S L L S A V L G .
GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG
1381 ----- + ----- + ----- + ----- + ----- + ----- + 1440
CTTAACCGGGGTTCAAGTGCCCCGACAGTCGCACGTACCTTCTTAACGGATACACAGAGTC

a E L A P S H G L V S V H G R I A Y V S Q .
CAGCCCTGGGTGTTCTCGGGAAGTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA
1441 ----- + ----- + ----- + ----- + ----- + ----- + 1500
GTCCGGACCCACAAGAGCCCTTGAGACTCCTCATTATAAAATAAACCCCTTCTTTATACTT

a Q P W V F S G T L R S N I L F G K K Y E .
AAGGAACGATATGAAAAAGTCATAAAGGCTTGCTGCTCTGAAAAAGGATTTACAGCTGTTG
1501 ----- + ----- + ----- + ----- + ----- + ----- + 1560
TTCCTTGCTATACTTTTTTCAGTATTTCCGAACACGAGACTTTTCTTAAATGTCGACAAC

a K E R Y E K V I K A C A L K K D L Q L L .
GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA
1561 ----- + ----- + ----- + ----- + ----- + ----- + 1620
CTCCTACCACTAGACTGACACTATCCTCTAGCCCCTTGGTGCGACTCACCTCCCGTCTTT

a E D G D L T V I G D R G T T L S G G Q K .
GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT
1621 ----- + ----- + ----- + ----- + ----- + ----- + 1680
CGTGCCCATTTGGAACGTTCTCGTCACATAGTTCTACGACTGTAGATAGAGGACCTGCTA

Figure 12D

18/56

a A R V N L A R A V Y Q D A D I Y L L D D -
CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTTGAAGTGTGTATTTGTCAA
1681 -----+-----+-----+-----+-----+-----+ 1740
GGAGAGTCACGTCATCTACGCCTTCAATCGTCTGTGAACAAGCTTGACACATAAACAGTT

a P L S A V D A E V S R H L F E L C I C O -
ATTTTGCATGAGAAGATCACAAATTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA
1741 -----+-----+-----+-----+-----+-----+ 1800
TAAAACGTACTCTTCTAGTGTTAAATCACTGAGTAGTCAACGTCATGGAGTTTCGACGT

a I L H E K I T I L V T H Q L Q Y L K A A -
AGTCAGATTCTGATATTGAAAGATGGTAAATGGTGCAGAAGGGGACTTACACTGAGTTC
1801 -----+-----+-----+-----+-----+-----+ 1860
TCAGTCTAAGACTATAACTTTCTACCATTTTACCACGTCTCCCCTGAATGTGACTCAAG

a S Q I L I L K D G K M V Q K G T Y T E F -
CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA
1861 -----+-----+-----+-----+-----+-----+ 1920
GATTTTAGACCATATCTAAAACCGAGGGAAAATTTCTTCTATTACTCCTTTCAGTTGTT

a L K S G I D F G S L L K K D N E E S E Q -
CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG
1921 -----+-----+-----+-----+-----+-----+ 1980
GGAGGTCAAGGTCCTTGAGGGTGTGATTCCTTAGCATGGAAGAGTCTCAGAAGCCAAACC

a P P V P G T P T L R N R T F S E S S V W -
TCTCAACAATCTTCTAGACCTCCTTGAAAGATGGTGTCTCTGGAGAGCCAAGATACAGAG
1981 -----+-----+-----+-----+-----+-----+ 2040
AGAGTTGTTAGAAGATCTGGGAGGAACTTCTACCACGAGACCTCTCGGTTCTATGTCTC

a S Q Q S S R P S L K D G A L E S Q D T E -
AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTTCAGGCC
2041 -----+-----+-----+-----+-----+-----+ 2100
TTACAGGGTCAATGTGATAGTCTCCTCTTGGAAGACTTCTTTTCAACCAAAAGTCCGG

a N V P V T L S E E N R S E G K V G F Q A

Figure 12E

SUBSTITUTE SHEET (RULE 26)

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19/56

TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA
 2101 -----+-----+-----+-----+-----+-----+ 2160
 ATATTCTTAATGAAGTCTCGACCACGAGTGACCTAACAGAAGTAAAAGGAATAAGAGGAT
 a Y K N Y F R A G A H W I V F I F L I L L -

AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC
 2161 -----+-----+-----+-----+-----+-----+ 2220
 TTGTGACGTGAGTCCAACGGATACACGAAGTTCTAACCACCGAAAGTATGACCCGTTTG
 a N T A A Q V A Y V L Q D W W L S Y W A N -

AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT
 2221 -----+-----+-----+-----+-----+-----+ 2280
 TTTGTTTCATACGATTTACAGTGACATTTACCTCCTCCTTTACATTGGCTCTTCGATCTA
 a K Q S M L N V T V N G G G N V T E K L D -

CTTAACTGGTACTTAGGAATTTATTACAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA
 2281 -----+-----+-----+-----+-----+-----+ 2340
 GAATTGACCATGAATCCTTAAATAAGTCCAAATTGACATCGATGGCAAGAAAAACCGTAT
 a L N W Y L G I Y S G L T V A T V L F G I -

GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAACTTTGCACAACAAA
 2341 -----+-----+-----+-----+-----+-----+ 2400
 CGTTCTAGAGATAACCATAAGATGCAGGAACAATTGAGAAGTGTTTGAAACGTGTTGTTT
 a A R S L L V F Y V L V N S S Q T L H N K -

ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA
 2401 -----+-----+-----+-----+-----+-----+ 2460
 TACAAACTCAGTTAAGACTTTCGAGGCCATAATAAGAACTATCTTTAGGTTATCCTTCT
 a M F E S I L K A P V L F F D R N P I G R -

ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT
 2461 -----+-----+-----+-----+-----+-----+ 2520
 TAAAAATTAGCAAAGAGGTTTCTGTAACCTGTGAACCTACTAAACGACGGCGACTGCAAA
 a I L N R F S K D I G H L D D L L P L T F

Figure 12F

WO 99/49735

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20/56

TTAGATTTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG
2521 -----+-----+-----+-----+-----+-----+ 2580
AATCTAAAGTAGGTCTGTAACGATGTTACCAACCAACCAGAGACACCGACACCGGCAC

a L D F I Q T L L Q V V G V V S V A V A V -

ATTCCTTGGATCGCAATACCCTTGGTTCCCTTGAATCATTTTCATTTTCTTCGGCGA
2581 -----+-----+-----+-----+-----+-----+ 2640
TAAGGAACCTAGCGTTATGGGAACCAAGGGGAACCTTAGTAAAAGTAAAAAGAAGCCGCT

a I P W I A I P I V P L G I I F I F L R R -

TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACCTCGGAGTCCAGTG
2641 -----+-----+-----+-----+-----+-----+ 2700
ATAAAAAACCTTTCAGTTCTCTACACTTCGCGGACCTTAGATGTTGAGCCTCAGGTCAC

a Y F L E T S R D V K R L E S T T R S P V -

TTTTCCCACTTGTCACTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA
2701 -----+-----+-----+-----+-----+-----+ 2760
AAAAGGGTGAACAGTAGAAGAGAGGTCCCCGAGACCTGGTAGGCCCGTATGTTTCGTCTT

a F S H L S S S L Q G L W T I R A Y K A E -

GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTGAGGCTTGGTTCTTG
2761 -----+-----+-----+-----+-----+-----+ 2820
CTCTCCACAGTCCTTGACAACTACGTGTGGTCTAAATGTAAGTCTCCGAACCAAGAAC

a E R C Q E L F D A H Q D L H S E A W F L -

TTTTTGACAACGTCCCGCTGGTTGCGCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC
2821 -----+-----+-----+-----+-----+-----+ 2880
AAAAACTGTTGCAGGGCGACCAAGCGGCAGGCAGACCTACGGTAGACACGGTACAAACAG

a F L T T S R W F A V R L D A I C A M F V -

ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT
2881 -----+-----+-----+-----+-----+-----+ 2940
TAGTAGCAACGGAAACCCAGGGACTAAGACCGTTTTTGAGACCTACGGCCCGTCCAACCA

a I I V A F G S L I L A K T L D A G Q V G -

TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTTCGACAAAGT

Figure 12G

SUBSTITUTE SHEET (RULE 26)

21/56

2941 -----+-----+-----+-----+-----+-----+ 3000
AACCGTGACAGGATACGGGAGTGCGAGTACCCCTACAAAGTCACCACACAAGCTGTTTCA

a L A L S Y A L T L M G M F Q W C V R Q S .

GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA
3001 -----+-----+-----+-----+-----+-----+ 3060
CGACTTCAACTCTTATACTACTAGAGTCATCTTTCCCAGTAACTTATGTGTCTGGAACCT

a A E V E N M M I S V E R V I E Y T D L E .

AAAGAAGCACCTTGGGAATATCAGAAACGCCACCACCAGCCTGGCCCCATGAAGGAGTG
3061 -----+-----+-----+-----+-----+-----+ 3120
TTTCTTCGTGGAACCCTTATAGTCTTTGCGGGTGGTGGTCCGACCGGGGTACTTCCTCAC

a K E A P W E Y Q K R P P P A W P H E G V .

ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT
3121 -----+-----+-----+-----+-----+-----+ 3180
TATTAGAACTGTTACACTTGAAGTACATGTCAGGTCCACCCGGAGACCATGACTTCGTA

a I I F D N V N F M Y S P G G P L V L K H .

CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA
3181 -----+-----+-----+-----+-----+-----+ 3240
GACTGTCGTGAGTAATTTAGTGTTCTTTTCCAACCGTAACACCCTTCTTGGCCTCGACCT

a L T A L I K S Q E K V G I V G R T G A G .

AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT
3241 -----+-----+-----+-----+-----+-----+ 3300
TTTTCAAGGGAGTAGAGTCGGGAAAAATCTAACAGTCTTGGGCTTCCATTTTAAACCTAA

a K S S L I S A L F R L S E P E G K I W I .

GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA
3301 -----+-----+-----+-----+-----+-----+ 3360
CTATTCTAGAACTGTTGACTTTAACCTGAAGTGCTAAATTCCTTCTTTTACAGTTAGTAT

a D K I L T T E I G L H D L R K K M S I I .

CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG
3361 -----+-----+-----+-----+-----+-----+ 3420

Figure 12H

22/56

GGAGTCCTTGGACAAAACAAGTGACCTTGTTACTCCTTTTTGGACCTAGGGAAATTCCTC

a P Q E P V L F T G T M R K N L D P F K E .

CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACCTTAAAGAAACCATTGAA

3421 ----- + ----- + ----- + ----- + ----- + ----- + 3480

GTGTGCCTACTCCTTGACACCTTACGGAATGTTCTCCATGTTGAATTTCTTTGGTAACTT

a H T D E E L W N A L Q E V O L K E T I E .

GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA

3481 ----- + ----- + ----- + ----- + ----- + ----- + 3540

CTAGAAGGACCATTTTACCTATGACTTAATCGTCTTAGTCCTAGGTTAAAATCACAACCT

a D L P G K M D T E L A E S G S N F S V G .

CAAAGACAACCTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT

3541 ----- + ----- + ----- + ----- + ----- + ----- + 3600

GTTTCTGTTGACCACACGGAACGGTCCCGTTAAGAGTCCTTTTTAGTCTATAACTAATAA

a Q R Q L V C L A R A I L R K N Q I L I I .

GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAAATCCGG

3601 ----- + ----- + ----- + ----- + ----- + ----- + 3660

CTACTTCGCTGCCGTTTACACCTAGGTTCTTGACTACTCAATTATGTTTTTTTTTAGGCC

a D E A T A N V D P R T D E L I Q K K I R .

GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC

3661 ----- + ----- + ----- + ----- + ----- + ----- + 3720

CTCTTTAAACGGGTGACGTGGCAGGATTGGTAACGTGTGTCTAACTTGTGGTAATAACTG

a E K F A H C T V L T I A H R L N T I I D .

AGCGACAAGATAATGGTTTTAGATTCAAGGAACTGAAAGAATATGATGAGCCGTATGTT

3721 ----- + ----- + ----- + ----- + ----- + ----- + 3780

TCGCTGTTCTATTACAAAATCTAAGTCCTTCTGACTTTCTTATACTACTCGGCATACAA

a S D K I M V L D S G R L K E Y D E P Y V .

TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACCTGGGCAAGGCAGAA

3781 ----- + ----- + ----- + ----- + ----- + ----- + 3840

AACGACGTTTTATTTCTCTCGGATAAAATGTTCTACCACGTTGTTGACCCGTTCCGTCTT

Figure 12I

23/56

a L L Q N K E S L F Y K M V Q Q L G K A E .

GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT
3841 -----+-----+-----+-----+-----+-----+ 3900
CGGCGACGGGAGTGACTTTGTCGTTTTGTCCATATGAAGTTTTCTTTAATAGGTGTATAA

a A A A L T E T A K Q V Y F K R N Y P H I .

GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT
3901 -----+-----+-----+-----+-----+-----+ 3960
CCAGTGTGACTGGTGTACCAATGTTTGTGAAGGTTACCTGTCGGGAGCTGGAATTGATAA

a G H T D H M V T N T S N G Q P S T L T I .

TTCGAGACAGCACTG
3961 -----+----- 3975
AAGCTCTGTCGTGAC

a F E T A L .

Figure 12J

24/56

MOAT C cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

ATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTG
1 -----+-----+-----+-----+-----+-----+ 60
TACTTCCTATAGCTGTATCCTTTTCTCATATAGTAGGGGTCAGGACCCATATCTTCACAC
a M K D I D I G K E Y I I P S P G Y R S V -

AGGGAGAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGA
61 -----+-----+-----+-----+-----+-----+ 120
TCCCTCTCTTGGTCGTGAAGACCCTGCGTGTCTCTGGCACTTCTAAGGTTCAAGTCCTCT
a R E R T S T S G T H R D R E D S K F R R -

ACTCGACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCT
121 -----+-----+-----+-----+-----+-----+ 180
TGAGCTGGCAACCTTACGGTTCTACGGAACCTTTGTCGTCGGGCTCGGCTCCCGGAGAGA
a T R P L E C Q D A L E T A A R A E G L S -

CTTGATGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAG
181 -----+-----+-----+-----+-----+-----+ 240
GAACTACGGAGGTACGTAAGAGTCGAGTCTTAGGACCTACTCCTCGTAGGGTTCCCTTTC
a L D A S M H S Q L R I L D E E H P K G K -

TACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCAGCACCCA
241 -----+-----+-----+-----+-----+-----+ 300
ATGGTAGTACCGAACTCACGAGACTTCGGGTAGGCCTGATGAAGGTTTGTGGTCGTGGGT
a Y H H G L S A L K P I R T T S K H Q H P -

GTGGACAATGCTGGGCTTTTTTCTGTATGACTTTTTCTGGGCTTTCTTCTCTGGCCCGT
301 -----+-----+-----+-----+-----+-----+ 360
CACCTGTTACGACCCGAAAAAAGGACATACTGAAAAAGCACCGAAAGAAGAGACCGGGCA
a V D N A G L F S C M T F S W L S S L A R -

GTGGCCCAACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAG

Figure 13A

WO 99/49735

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361 -----+-----+-----+-----+-----+-----+ 420
CACCGGGTGTCTTCCCCCTCGAGAGTTACCTTCTGCACACCAGAGACAGGTTCTGTGCTC

a V A H K K G E L S M E D V W S L S K H E .

TCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTT

421 -----+-----+-----+-----+-----+-----+ 480
AGAAGACTGCACTTGACGTCTTCTGATCTCTCTGACACCGTTCTTCTCGACTTACTTCAA

a S S D V N C R R L E R L W Q E E L N E V .

GGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATC

481 -----+-----+-----+-----+-----+-----+ 540
CCCGGTCTGCGACGAAGGGACGCTTCCCAACACACCTAGAAGACGGCGTGGTCCGAGTAG

a G P D A A S L R R V V W I F C R T R L I .

CTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATG

541 -----+-----+-----+-----+-----+-----+ 600
GACAGGTAGCACACGGACTACTAGTGCCTGACCGACCGAAGTCACCTGGTCGGAAGTAC

a L S I V C L M I T Q L A G F S G P A F M .

GTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTG

601 -----+-----+-----+-----+-----+-----+ 660
CACTTTGTGGAGAACCTCATATGGGTCCGTTGTCTCAGATTGGACGTCATGTGGAACAAC

a V K H L L E Y T Q A T E S N L Q Y S L L .

TTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGG

661 -----+-----+-----+-----+-----+-----+ 720
AATCAGACCCGGAGGAGGACTGCCTTTAGCACGCCAGAACCAGCGAACGTGACTGAACC

a L V L G L L L T E I V R S W S L A L T W .

GCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAG

721 -----+-----+-----+-----+-----+-----+ 780
CGTAACTTAATGGCTTGCCACAGGCGAACGCCCCCGGTAGGATTGGTACCGTAAATTC

a A L N Y R T G V R L R G A I L T M A F K .

AAGATCCTTAAGTTAAAGAACAATTAAGAGAAATCCCTGGGTGAGCTCATCAACATTTC

781 -----+-----+-----+-----+-----+-----+ 840

Figure 13B

SUBSTITUTE SHEET (RULE 26)

26/56

TTCTAGGAATTCAATTTCTTGTAATTTCTCTTTAGGGACCCACTCGAGTAGTTGTAAACG

a K I L K L K N I K E K S L G E L I N I C -

TCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGA

841 -----+-----+-----+-----+-----+-----+ 900

AGGTTGCTACCCGCTCTTACAAACTCCGTCGTCGGCAACCGTCGGACGACCGACCTCCT

a S N D G O R M F E A A A V G S L L A G G -

CCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTC

901 -----+-----+-----+-----+-----+-----+ 960

GGGCAACAACGGTAGAATCCGTACTAAATATTACATTAATAAGACCCTGGTTGTCCGAAG

a P V V A I L G M I Y N V I I L G P T G F -

CTGGGATCAGCTGTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACA

961 -----+-----+-----+-----+-----+-----+ 1020

GACCCTAGTCGACAAAAATAGGAGAAAATGGGTCGTTACTACAAACGTAGTGCCGAGTGT

a L G S A V F I L F Y P A M M F A S R L T -

GCATATTTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAA

1021 -----+-----+-----+-----+-----+-----+ 1080

CGTATAAAGTCCTCTTTTACGCACCGGCGGTGCCTACTTGACAGGTCTTCTACTTACTT

a A Y F R R K C V A A T D E R V Q K M N E -

GTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGT

1081 -----+-----+-----+-----+-----+-----+ 1140

CAAGAATGAATGTAATTTAAATAGTTTTACATACGGACCCAGTTTCGTAAAAGAGTCTCA

a V L T Y I K F I K M Y A W V K A F S Q S -

GTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGGGT

1141 -----+-----+-----+-----+-----+-----+ 1200

CAAGTCTTTTAGGCGCTCCTCCTCGCAGCCTATAACCTTTTTTCGGCCCATGAAGGTCCCA

a V Q K I R E E E R R I L E K A G Y F Q G -

ATCACTGTGGGTGTGGCTCCCATTTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTT

1201 -----+-----+-----+-----+-----+-----+ 1260

TAGTGACACCCACACCGAGGGTAACACCACCACTAACGGTCGCACCACTGGAAGAGACAA

Figure 13C

27/56

a I T V G V A P I V V V I A S V V T F S V .
CATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTTCACAGTGGTGACAGTCTTC
1261 -----+-----+-----+-----+-----+ 1320
GTATACTGGGACCCGAAGCTAGACTGTCGTCGTGCCGAAAGTGTCACCACTGTCAGAAG

a H M T L G F D L T A A Q A F T V V T V F .
AATCCATGACTTTTGCTTGAAAGTAACACCGTTTTTCAGTAAAGTCCCTCTCAGAAGCC
1321 -----+-----+-----+-----+-----+ 1380
TTAAGGTACTGAAAACGAACTTTCATTGTGGCAAAAGTCATTTTCAGGGAGAGTCTTCGG

a N S M T F A L K V T P F S V K S L S E A .
TCAGTGGCTGTTGACAGATTTAAGAGTTTGTCTTAATGGAAGAGGTTACATGATAAAG
1381 -----+-----+-----+-----+-----+ 1440
AGTCACCGACAACGTCTAAATTCTCAAACAAAGATTACCTTCTCCAAGTGACTATTTTC

a S V A V D R F K S L F L M E E V H M I K .
AACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGAC
1441 -----+-----+-----+-----+-----+ 1500
TTGTTTGGTCGGTCAGGAGTGAGTTCTATCTCTACTTTTTACGGTGGAACCGTACCCTG

a N K P A S P H I K I E M K N A T L A W D .
TCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAG
1501 -----+-----+-----+-----+-----+ 1560
AGGAGGGTGAGGTCATAGGTCTTGAGCGGGTTCGACTGGGGGTTTTACTTTTTCTGTTC

a S S H S S I O N S P K L T P K M K K D K .
AGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCG
1561 -----+-----+-----+-----+-----+ 1620
TCCCGAAGGTCCCCGTTCTTTCTCTTCCACTCCGTCGACGTCGCGTGACTCGTAGTCCGC

a R A S R G K K E K V R Q L Q R T E H Q A .
GTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCAGTCCCGAA
1621 -----+-----+-----+-----+-----+ 1680
CACGACCGTCTCGTCTTTCCGGTGAGGAGGACCTGTCACTGCTCGCCGGGTCAGGGCTT

Figure 13D

WO 99/49735

PCT/US99/06644

28/56

a V L A E O K G H L L L D S D E R P S P E .
GAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGC
1681 -----+-----+-----+-----+-----+-----+ 1740
CTCCTTCTCCGTTTCGTGTAGGTGGACCCGGTGGACGCGAATGTCTCCTGTGACGTGTCG

a E E E G K H I H L G H L R L O R T L H S .
ATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGA
1741 -----+-----+-----+-----+-----+-----+ 1800
TAGCTAGACCTCTAGGTTCTCCCATTTGACCAACCTTAGACGCCGTCACACCCTTCACCT

a I D L E I Q E G K L V G I C G S V G S G .
AAAACCTCTCTCATTTAGCCATTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCA
1801 -----+-----+-----+-----+-----+-----+ 1860
TTTTGGAGAGAGTAAAGTCGGTAAAATCCGGTCTACTGCGAAGATCTCCCGTCGTAACGT

a K T S L I S A I L G O M T L L E G S I A .
ATCAGTGGAACCTTCGCTTATGTGGCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGA
1861 -----+-----+-----+-----+-----+-----+ 1920
TAGTCACCTTGAAGCGAATACACCGGGTCGTCCGGACCTAGGAGTTACGATGAGACTCT

a I S G T F A Y V A Q Q A W I L N A T L R .
GACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACTCTGTGCTGAACAGC
1921 -----+-----+-----+-----+-----+-----+ 1980
CTGTTGTAGGACAAACCCTTCCTTATACTACTTCTTTCTATGTTGAGACACGACTTGTCG

a D N I L F G K E Y D E E R Y N S V L N S .
TGCTGCCTGAGGCCTGACCTGGCCATTCTTCCAGCAGCGACCTGACGGAGATTGGAGAG
1981 -----+-----+-----+-----+-----+-----+ 2040
ACGACGGACTCCGGACTGGACCGTAAGAAGGGTCGTGCTGGACTGCCTCTAACCTCTC

a C C L R P D L A I L P S S D L T E I G E .
CGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGAT
2041 -----+-----+-----+-----+-----+-----+ 2100
GCTCCTCGGTTGGACTCGCCACCGTCGCGGTCTCCTAGTCGGAACGGGCCCCGGAACATA

a R G A N L S G G O R O R I S L A R A L Y .

Figure 13E

SUBSTITUTE SHEET (RULE 26)

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AGTGACAGGAGCATCTACATCCTGGACGACCCCTCAGTGCCTTAGATGCCCATGTGGGC
2101 -----+-----+-----+-----+-----+-----+ 2160
TCACTGTCCTCGTAGATGTAGGACCTGCTGGGGGAGTCACGGAATCTACGGGTACACCCG

a S D R S I Y I L D D P L S A L D A H V G .

AACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGT
2161 -----+-----+-----+-----+-----+-----+ 2220
TTGGTGTAGAAGTTATCACGATAGGCCTTTGTAGAGTTCAGGTTCTGTCAAGACAAACAA

a N H I F N S A I R K H L K S K T V L F V .

ACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGT
2221 -----+-----+-----+-----+-----+-----+ 2280
TGGGTGGTCAATGTCATGGACCAACTGACACTACTTCACTAGAAGTACTTTCTCCCGACA

a T H Q L Q Y L V D C D E V I F M K E G C .

ATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATT
2281 -----+-----+-----+-----+-----+-----+ 2340
TAATGCCTTTCTCCGTGGGTACTCCTTGACTACTTAAATTTACCACTGATACGATGGTAA

a I T E R G T H E E L M N L N G D Y A T I .

TTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACC
2341 -----+-----+-----+-----+-----+-----+ 2400
AAATTATTGGACAACGACCCTCTCTGTGGCGGTCAACTCTAGTTAAGTTTTTCTTTGG

a F N N L L L G E T P P V E I N S K K E T .

AGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCTTAAACAGGATCAGTAAAGAAGGAA
2401 -----+-----+-----+-----+-----+-----+ 2460
TCACCAAGTGTCTTCTTCAGTGTTCTGTTCCAGGATTTTGTCTAGTCATTTCTTCCTT

a S G S Q K K S Q D K G P K T G S V K K E .

AAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCA
2461 -----+-----+-----+-----+-----+-----+ 2520
TTTCGTCATTTCCGGTCTCCTTCCCGTCGAACACGTCGACCTTCTCTTTCCCGTCCCAAGT

a K A V K P E E G O L V O L E E K G O G S .

Figure 13F

SUBSTITUTE SHEET (RULE 26)

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GTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCTTGGCATTCTCTG
2521 -----+-----+-----+-----+-----+-----+ 2580
CACGGGACCAGTCATATACACAGATGTAGGTCCGACGACCCCCGGGAACCGTAAGGAC

a V P W S V Y G V Y I Q A A G G P L A F L .

GTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTG
2581 -----+-----+-----+-----+-----+-----+ 2640
CAATAATACCGGGAAGTACGACTTACATCCGTCCTGGCGGAAGTCGTGGACCACCAAC

a V I M A L F M L N V G S T A F S T W W L .

AGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCG
2641 -----+-----+-----+-----+-----+-----+ 2700
TCAATGACCTAGTTCGTTCTTCGCCCTTGTGGTGACACTGAGCTCCCTTGCTCTGGAGC

a S Y W I K Q G S G N T T V T R G N E T S .

GTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTC
2701 -----+-----+-----+-----+-----+-----+ 2760
CACTCACTGTCGTA CTCTCTGTTAGGAGTATACGTCATGATACGGTCGTAGATGCGGGAG

a V S D S M K D N P H M Q Y Y A S I Y A L .

TCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACG
2761 -----+-----+-----+-----+-----+-----+ 2820
AGGTACCGTCAGTACGACTAGGACTTTGCGTAAGCTCCTCAACAGAAACAGTTCCCGTGC

a S M A V M L I L K A I R G V V F V K G T .

CTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATG
2821 -----+-----+-----+-----+-----+-----+ 2880
GACGCTCGAAGGAGGGCCGACGTA CTGCTCGAAAAGGCTTCCTAGGAAGCTTCGGGATAC

a L R A S S R L H D E L F R R I L R S P M .

AAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGAT
2881 -----+-----+-----+-----+-----+-----+ 2940
TTCAAAAAA CTGTGCTGGGGGTGTCCCTCCTAAGAGTTGTCCAAAAGGTTTCTGTACCTA

a K F F D T T P T G R I L N R F S K D M D .

GAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTTCATCCAGAACGTTATCCTGGTG

Figure 13G

SUBSTITUTE SHEET (RULE 26)

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2941 -----+-----+-----+-----+-----+-----+ 3000
CTTCAACTGCACGCCGACGGCAAGGTCCGGCTCTACAAGTAGGTCTTGCAATAGGACCAC
a E V D V R L P F Q A E M F I Q N V I L V -

TTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCC
3001 -----+-----+-----+-----+-----+-----+ 3060
AAGAAGACACACCCTTACTAGCGTCCTCAGAAGGGCACCAAGGAACACCGTCACCCCGGG
a F F C V G M I A G V F P W F L V A V G P -

CTTGTCACTCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCTGATTCGGGAGCTGAAG
3061 -----+-----+-----+-----+-----+-----+ 3120
GAACAGTAGGAGAAAAGTCAGGACGTGTAACAGAGGTCCCAGGACTAAGCCCTCGACTTC
a L V I L F S V L H I V S R V L I R E L K -

CGTCTGGACAATATCACGCAGTCACCTTCTCTCCACATCACGTCCAGCATAACAGGGC
3121 -----+-----+-----+-----+-----+-----+ 3180
GCAGACCTGTTATAGTGCGTCAGTGGAAAGGAGAGGGTGTAGTGCAGGTCGTATGTCCCG
a R L D N I T Q S P F L S H I T S S I Q G -

CTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTG
3181 -----+-----+-----+-----+-----+-----+ 3240
GAACGGTGGTAGGTGCGGATGTTATTTCCCGTCCTCAAAGACGTGTCTATGGTCCTCGAC
a L A T I H A Y N K G Q E F L H R Y Q E L -

CTGGATGACAACCAAGCTCCTTTTTTTTTTGTTCACGTGTGCGATGCGGTGGCTGGCTGTG
3241 -----+-----+-----+-----+-----+-----+ 3300
GACCTACTGTTGGTTCGAGGAAAAAAAAACAAATGCACACGCTACGCCACCGACCGACAC
a L D D N Q A P F F L F T C A M R W L A V -

CGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATG
3301 -----+-----+-----+-----+-----+-----+ 3360
GCCGACCTGGAGTAGTCGTAGCGGGAGTAGTGGTGGTGCCCCGACTACTAGCAAGAATAC
a R L D L I S I A L I T T T G L M I V L M -

CACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACG
3361 -----+-----+-----+-----+-----+-----+ 3420

Figure 13H

SUBSTITUTE SHEET (RULE 26)

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GTGCCCCGTCTAAGGGGGTCGGATACGCCCAGAGCGGTAGAGAATACGACAGGTCAATTGC

a H G O I P P A Y A G L A I S Y A V O L T .

GGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTACCTCGGTG
3421 ----- + ----- + ----- + ----- + ----- + ----- + 3480
CCCGACAAGGTCAAATGCCAGTCTGACCGTAGACTCTGTCTTCGAGCTAAGTGGAGCCAC

a G L F O F T V R L A S E T E A R F T S V .

GAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAAC
3481 ----- + ----- + ----- + ----- + ----- + ----- + 3540
CTCTCCTAGTTAGTGATGTAATTCTGAGACAGGAACCTTCGTGGACGGTCTTAATTCTTG

a E R I N H Y I K T L S L E A P A R I K N .

AAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATG
3541 ----- + ----- + ----- + ----- + ----- + ----- + 3600
TTCCGAGGGAGGGGACTGACCGGGGTCTCCCTCTCCACTGGAACTCTTGCGTCTCTAC

a K A P S P D W P Q E G E V T F E N A E M .

AGGTACCGAGAAAACCTCCCTCTTGTCTAAAGAAAGTATCCTTCACGATCAAACCTAAA
3601 ----- + ----- + ----- + ----- + ----- + ----- + 3660
TCCATGGCTCTTTTGGAGGGAGAACAGGATTTCTTTCATAGGAAGTGCTAGTTTGGATT

a R Y R E N L P L V L K K V S F T I K P K .

GAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTC
3661 ----- + ----- + ----- + ----- + ----- + ----- + 3720
CTCTTCTAACCGTAACACCCCGCCTGTCTAGTCCCTTCAGGAGCGACCCCTACCGGGAG

a E K I G I V G R T G S G K S S L G M A L .

TTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGAT
3721 ----- + ----- + ----- + ----- + ----- + ----- + 3780
AAGGCAGACCACCTCAATAGACCTCCGACGTAGTTCTAACTACCTCACTCTTAGTCACTA

a F R L V E L S G G C I K I D G V R I S D .

ATTGGCCTTGCCGACCTCCGAAGCAAACCTCTATCATTCCTCAAGAGCCGGTGCTGTTT
3781 ----- + ----- + ----- + ----- + ----- + ----- + 3840
TAACCGGAACGGCTGGAGGCTTCGTTTGAGAGATAGTAAGGAGTTCTCGGCCACGACAAG

Figure 13I

33/56

a I G L A D L R S K L S I I P Q E P V L F -
 AGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGG
 3841 -----+-----+-----+-----+-----+-----+ 3900
 TCACCGTGACAGTCTAGTTTAAACCTGGGGAAGTTGGTCATGTGACTTCTGGTCTAAACC

a S G T V R S N L D P F N O Y T E D O I W -
 GATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAA
 3901 -----+-----+-----+-----+-----+-----+ 3960
 CTACGGGACCTCTCCTGTGTGTACTTTCTTACATAACGAGTCGATGGAGACTTTGAACTT

a D A L E R T H M K E C I A Q L P L K L E -
 TCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATA
 3961 -----+-----+-----+-----+-----+-----+ 4020
 AGACTTCACTACCTCTTACCCCTATTGAAGAGTCACCCCTTGCCGTCGAGAACACGTAT

a S E V M E N G D N F S V G E R Q L L C I -
 GCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATG
 4021 -----+-----+-----+-----+-----+-----+ 4080
 CGATCTCGGGACGAGGCGGTGACATTCTAAGACTAAATCTACTTCGGTGTGACGGTAC

a A R A L L R H C K I L I L D E A T A A M -
 GACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTCAGACTGTACC
 4081 -----+-----+-----+-----+-----+-----+ 4140
 CTGTGTCTCTGTCTGAATAACTAAGTTCTCTGGTAGGCTCTTCGTAAACGTCTGACATGG

a D T E T D L L I Q E T I R E A F A D C T -
 ATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTG
 4141 -----+-----+-----+-----+-----+-----+ 4200
 TACGACTGGTAACGGGTAGCGGACGTGTGCCAAGATCCGAGGCTATCCTAATACCACGAC

a M L T I A H R L H T V L G S D R I M V L -
 GCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCC
 4201 -----+-----+-----+-----+-----+-----+ 4260
 CGGGTCCCTGTCCACCACCTCAAACCTGTGGGGTAGCCAGGAAGACAGGTTGCTGTCAAGG

Figure 13J

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a A Q G Q V V E F D T P S V L L S N D S S .

CGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGA
4261 -----+-----+-----+-----+-----+---- 4314
GCTAAGATACGGTACAAACGACGACGTCTCTTGTTCAGCGACAGTTCCCGACT

a R F Y A M F A A A E N K V A V K G .

Figure 13K

SUBSTITUTE SHEET (RULE 26)

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MOAT D cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

ATGGACGCCCTGTGCGGTTCCGGGGAGCTCGGCTCCAAGTTCTGGGACTCCAACCTGTCT
 1 -----+-----+-----+-----+-----+-----+ 60
 TACCTGCGGGACACGCCAAGGCCCTCGAGCCGAGGTTCAAGACCCTGAGGTTGGACAGA
 a M D A L C G S G E L G S K F W D S N L S .

GTGCACACAGAAAACCCGGACCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCCTGGGTG
 61 -----+-----+-----+-----+-----+-----+ 120
 CACGTGTGTCTTTTGGGCTGGAGTGAGGGACGAAGGTCTTGAGGGACGACCGGACCCAC
 a V H T E N P D L T P C F Q N S L L A W V .

CCCTGCATCTACCTGTGGGTCGCCCTGCCCTGCTACTTGCTCTACCTGCGGCACCATGT
 121 -----+-----+-----+-----+-----+-----+ 180
 GGGACGTAGATGGACACCCAGCGGGACGGGACGATGAACGAGATGGACGCCGTGGTAACA
 a P C I Y L W V A L P C Y L L Y L R H H C .

CGTGGCTACATCATCCTCTCCACCTGTCCAAGCTCAAGATGGTCCTGGGTGTCCTGCTG
 181 -----+-----+-----+-----+-----+-----+ 240
 GCACCGATGTAGTAGGAGAGGGTGGACAGGTTCTGAGTTCTACCAGGACCCACAGGACGAC
 a R G Y I I L S H L S K L K M V L G V L L .

TGGTGCGTCTCCTGGGCGGACCTTTTTTACTCCTTCCATGGCCTGGTCCATGGCCGGGCC
 241 -----+-----+-----+-----+-----+-----+ 300
 ACCACGCAGAGGACCCGCCTGGAAAAAATGAGGAAGGTACCGGACCAGGTACCGGCCCGG
 a W C V S W A D L F Y S F H G L V H G R A .

CTGCCCCCTGTTTTCTTTGTCACCCCTTGGTGGTGGGGGTCACCATGCTGCTGGCCACC
 301 -----+-----+-----+-----+-----+-----+ 360
 GGACGGGGACAAAAGAAACAGTGGGGGAACCACCACCCCAAGTGGTACGACGACCGGTGG
 a P A P V F F V T P L V V G V T M L L A T .

CTGCTGATACAGTATGAGCGGCTGCAGGGCGTACAGTCTTCGGGGGTCCTCATTATCTTC

Figure 14A

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361 -----+-----+-----+-----+-----+-----+ 420
GACGACTATGTCATACTCGCCGACGTCCCGCATGTCAGAAGCCCCCAGGAGTAATAGAAG

a L L I Q Y E R L Q G V Q S S G V L I I F -

TGGTTCCTGTGTGTGGTCTGCGCCATCGTCCCATTCGCTCCAAGATCCTTTAGCCAAG

421 -----+-----+-----+-----+-----+-----+ 480
ACCAAGGACACACACCAGACGCGGTAGCAGGGTAAGGCGAGGTTCTAGGAAAATCGGTTTC

a W F L C V V C A I V P F R S K I L L A K -

GCAGAGGGTGAGATCTCAGACCCCTTCCGCTTCACCACCTTCTACATCCACTTTGCCCTG

481 -----+-----+-----+-----+-----+-----+ 540
CGTCTCCCACTCTAGAGTCTGGGGAAGGCGAAGTGGTGGAAGATGTAGGTGAAACGGGAC

a A E G E I S D P F R F T T F Y I H F A L -

GTA CTCTCTGCCCTCATCTTGGCCTGCTTCAGGGAGAAACCTCCATTTTCTCCGCAAAG

541 -----+-----+-----+-----+-----+-----+ 600
CATGAGAGACGGGAGTAGAACC GGACGAAGTCCCTCTTTGGAGGTAAAAAGAGGCGTTTC

a V L S A L I L A C F R E K P P F F S A K -

AATGTCGACCCTAACCCTACCCTGAGACCAGCGCTGGCTTTCTCTCCCGCCTGTTTTTC

601 -----+-----+-----+-----+-----+-----+ 660
TTACAGCTGGGATTGGGGATGGGACTCTGGTCGCGACCGAAAGAGAGGGCGGACAAAAAG

a N V D P N P Y P E T S A G F L S R L F F -

TGGTGTTTCACAAAGATGGCCATCTATGGCTACCGGCATCCCCTGGAGGAGAAGGACCTC

661 -----+-----+-----+-----+-----+-----+ 720
ACCACCAAGTGTTCCTACCGGTAGATACCGATGGCCGTAGGGGACCTCCTCTTCCTGGAG

a W W F T K M A I Y G Y R H P L E E K D L -

TGGTCCCTAAAGGAAGAGGACAGATCCCAGATGGTGGTGCAGCAGCTGCTGGAGGCATGG

721 -----+-----+-----+-----+-----+-----+ 780
ACCAGGGATTTCCTTCTCCTGTCTAGGGTCTACCACCACGTCGTCGACGACCTCCGTACC

a W S L K E E D R S Q M V V Q O L L E A W -

AGGAAGCAGGAAAAGCAGACGGCACGACACAAGGCTTCAGCAGCACCTGGGAAAAATGCC

781 -----+-----+-----+-----+-----+-----+ 840

Figure 14B

SUBSTITUTE SHEET (RULE 26)

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TCCTTCGTCCTTTTCGTCTGCCGTGCTGTGTTCCGAAGTCGTCTGGACCCTTTTACGG

a R K Q E K Q T A R H K A S A A P G K N A .

TCCGGCGAGGACGAGGTGCTGCTGGGTGCCCCGCCAGGCCCGGAAGCCCTCCTTCCTG

841 -----+-----+-----+-----+-----+-----+ 900

AGGCCGCTCCTGCTCCACGACGACCCACGGGCCGGTCCGGGGCCTTCGGGAGGAAGGAC

a S G E D E V L L G A R P R P R K P S F L .

AAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAGTGCCTGCTTCAAGCTTATC

901 -----+-----+-----+-----+-----+-----+ 960

TTCCGGGACGACCGGTGGAAGCCGAGGTGGAAGGAGTAGTCACGGACGAAGTTCGAATAG

a K A L L A T F G S S F L I S A C F K L I .

CAGGACCTGCTCTCCTTCATCAATCCACAGCTGCTCAGCATCCTGATCAGGTTTATCTCC

961 -----+-----+-----+-----+-----+-----+ 1020

GTCCTGGACGAGAGGAAGTAGTTAGGTGTGACGAGTCGTAGGACTAGTCCAAATAGAGG

a Q D L L S F I N P Q L L S I L I R F I S .

AACCCCATGGCCCCCTCCTGGTGGGGCTTCCTGGTGGCTGGGGCTGATGTTCTGTGCTCC

1021 -----+-----+-----+-----+-----+-----+ 1080

TTGGGGTACCGGGGGAGGACCACCCCGAAGGACCACCGACCCGACTACAAGGACACGAGG

a N P M A P S W W G F L V A G L M F L C S .

ATGATGCAGTCGCTGATCTTACAACACTATTACCACTACATCTTTGTGACTGGGGTGAAG

1081 -----+-----+-----+-----+-----+-----+ 1140

TACTACGTCAGCGACTAGAATGTTGTGATAATGGTGATGTAGAAACACTGACCCCACTTC

a M M Q S L I L Q H Y Y H Y I F V T G V K .

TTTCGTA TGGGATCATGGGTGTCATCTACAGGAAGGCTCTGGTTATCACCAACTCAGTC

1141 -----+-----+-----+-----+-----+-----+ 1200

AAAGCATGACCCTAGTACCCACAGTAGATGTCCTTCCGAGACCAATAGTGGTTGAGTCAG

a F R T G I M G V I Y R K A L V I T N S V .

AAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTCAGTGGATGCCAGCGCTTC

1201 -----+-----+-----+-----+-----+-----+ 1260

TTTGACGCGAGGTGACACCCCTTTAACAGTTGGAGTACAGTCACCTACGGGTCGCGAAG

Figure 14C

a K R A S T V G E I V N L M S V D A Q R F -
ATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGTCAGCACCCCTGCAGATCATCCTGGCG
1261 -----+-----+-----+-----+-----+-----+ 1320
TACCTGGAACGGGGAAGGAGTTAGACGACACCAGTCGTGGGGACGTCTAGTAGGACCGC

a M D L A P F L N L L W S A P L Q I I L A -
ATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGCTGGAGTCGCTTTCATGGTC
1321 -----+-----+-----+-----+-----+-----+ 1380
TAGATGAAGGAGACCGTCTTGGATCCAGGGAGACAGGACCGACCTCAGCGAAAGTACCAG

a I Y F L W Q N L G P S V L A G V A F M V -
TTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCGCGCCTTCCAGGTAAAGCAA
1381 -----+-----+-----+-----+-----+-----+ 1440
AACGACTAAGGTGAGTTGCCTCGACACCGGCACTTCTACGCGCGGAAGGTCCATTTGTT

a L L I P L N G A V A V K M R A F Q V K Q -
ATGAAATTGAAGGACTCGCGCATCAAGCTGATGAGTGAGATCCTGAACGGCATCAAGGTG
1441 -----+-----+-----+-----+-----+-----+ 1500
TACTTTAACTTCCTGAGCGCGTAGTTCGACTACTCACTCTAGGACTTGCCGTAGTTCAC

a M K L K D S R I K L M S E I L N G I K V -
CTGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGTGGAGGGCATCCGGCAGGGT
1501 -----+-----+-----+-----+-----+-----+ 1560
GACTTCGACATGCGGACCCTCGGGTCGAAGGACTTCGTCCACCTCCCGTAGGCCGTCCCA

a L K L Y A W E P S F L K Q V E G I R Q G -
GAGCTCCAGCTGCTGCGCACGGCGGCCTACCTCCACACCACAACCACCTTCACCTGGATG
1561 -----+-----+-----+-----+-----+-----+ 1620
CTCGAGGTGACGACGCGTGCCGCCGATGGAGGTGTGGTGTGGTGGGAAGTGGACCTAC

a E L Q L L R T A A Y L H T T T T F T W M -
TGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTACGTGTACGTGGACCCAAAC
1621 -----+-----+-----+-----+-----+-----+ 1680
ACGTGCGGGAAGGACCACTGGGACTAGTGGGAGACCCACATGCACATGCACCTGGGTTTG

Figure 14D

a C S P F L V T L I T L W V Y V Y V D P N -
AATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCTTGTTTAATATCTTAAGACTT
1681 -----+-----+-----+-----+-----+-----+ 1740
TTACACGACCTGCGGCTCTTCCGGAAACACAGACACAGGAACAAATTATAGAATTCTGAA

a N V L D A E K A F V S V S L F N I L R L -
CCCCCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCAGGCCAGTGTGTCTCTGAAA
1741 -----+-----+-----+-----+-----+-----+ 1800
GGGGAGTTGTACGACGGGGTCAATTAGTCGTTGGACTGAGTCCGGTCACACAGAGACTTT

a P L N M L P Q L I S N L T Q A S V S L K -
CGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCAGAGTGTGGAAAGAAAGACC
1801 -----+-----+-----+-----+-----+-----+ 1860
GCCTAGGTCGTTAAGGACTCGGTTCTCCTTGAAGTGGGGTCTCACACCTTTCTTTCTGG

a R I Q Q F L S Q E E L D P Q S V E R K T -
ATCTCCCCAGGCTATGCCATCACCATACACAGTGGCACCTTCACCTGGGCCAGGACCTG
1861 -----+-----+-----+-----+-----+-----+ 1920
TAGAGGGGTCCGATACGGTAGTGGTATGTGTACCGTGGAAAGTGGACCCGGGTCTGGAC

a I S P G Y A I T I H S G T F T W A Q D L -
CCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGCACTGGTGGCCGTGGTG
1921 -----+-----+-----+-----+-----+-----+ 1980
GGGGGGTGAGACGTGTGCGATCTGTAGGTCCAGGGCTTTCCCCGTGACCACCGGCACCAC

a P P T L H S L D I Q V P K G A L V A V V -
GGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGTGTCTGCCCTGCTGGGAGAGATGGAGAAG
1981 -----+-----+-----+-----+-----+-----+ 2040
CCCGGACACCCGACACCCTTCAGGAGGGACCACAGACGGGACGACCCTCTCTACCTCTTC

a G P V G C G K S S L V S A L L G E M E K -
CTAGAAGGCCAAAGTGACATGAAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTG
2041 -----+-----+-----+-----+-----+-----+ 2100
GATCTTCCGTTTCACGTGTACTTCCGTACCTAGGTCTTGACGTGAGAAGTCCTTTTGAC

a L E G K V H M K A W I Q N C T L Q E N V -

Figure 14E

SUBSTITUTE SHEET (RULE 26)

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CTTTTCGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTG
2101 -----+-----+-----+-----+-----+-----+ 2160
GAAAAGCCGTTTCGGGACTTGGGGTTCGCGATGGTCGTCTGAGACCTCCGGACACGGAAC

a L F G K A L N P K R Y Q Q T L E A C A L -

CTAGCTGACCTGGAGATGCTGCCTGGTGGGGATCAGACAGAGATTGGAGAGAAGGGCATT
2161 -----+-----+-----+-----+-----+-----+ 2220
GATCGACTGGACCTCTACGACGGACCAACCCCTAGTCTGTCTCTAACCTCTCTTCCCGTAA

a L A D L E M L P G G D Q T E I G E K G I -

AACCTGTCTGGGGGCCAGCGGCAGCGGGTCACTCTGGCTCGAGCTGTTTACAGTGATGCC
2221 -----+-----+-----+-----+-----+-----+ 2280
TTGGACAGACCCCCGGTCGCCGTCGCCAGTCAGACCGAGCTCGACAAATGTCACTACGG

a N L S G G Q R Q R V S L A R A V Y S D A -

GATATTTTCTTGCTGGATGACCCACTGTCCGCGGTGGACTCTCATGTGGCCAAGCACATC
2281 -----+-----+-----+-----+-----+-----+ 2340
CTATAAAAGAACGACCTACTGGGTGACAGGCGCCACCTGAGAGTACACCGGTTCTGTAG

a D I F L L D D P L S A V D S H V A K H I -

TTTGACCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGAGTGCTGGTGACG
2341 -----+-----+-----+-----+-----+-----+ 2400
AAACTGGTGACGTAGCCCGGTCTTCCGCACGACCGTCCGTTCTGCGCTCACGACCACTGC

a F D H V I G P E G V L A G K T R V L V T -

CACGGCATTAGCTTCCTGCCCCAGACAGACTTCATCATTGTGCTAGCTGATGGACAGGTG
2401 -----+-----+-----+-----+-----+-----+ 2460
GTGCCGTAATCGAAGGACGGGGTCTGTCTGAAGTAGTAACACGATCGACTACCTGTCCAC

a H G I S F L P Q T D F I I V L A D G Q V -

TCTGAGATGGGCCCCGTACCCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTC
2461 -----+-----+-----+-----+-----+-----+ 2520
AGACTCTACCCGGGCATGGGTCTGGGACGACGTGCGGTTGCCGAGGAAACGGTTGAAAGAG

a S E M G P Y P A L L Q R N G S F A N F L -

Figure 14F

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TGCAACTATGCCCCGATGAGGACCAAGGGCACCTGGAGGACAGCTGGACCGCGTTGGAA
 2521 -----+-----+-----+-----+-----+-----+ 2580
 ACGTTGATACGGGGGCTACTCCTGGTTCCCGTGGACCTCCTGTCGACCTGGCGCAACCTT
 a C N Y A P D E D Q G H L E D S W T A L E .

GGTGCAGAGGATAAGGAGGCACTGCTGATTGAAGACACACTCAGCAACCACACGGATCTG
 2581 -----+-----+-----+-----+-----+-----+ 2640
 CCACGTCTCCTATTCTCCTCCGTGACGACTAACTTCTGTGTGAGTCGTTGGTGTGCCTAGAC
 a G A E D K E A L L I E D T L S N H T D L .

ACAGACAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCC
 2641 -----+-----+-----+-----+-----+-----+ 2700
 TGTCTGTTACTAGGTCACTGGATACACCAGGTCTTCGTCAAATACTCTGTGCACTCACGG
 a T D N D P V T Y V V Q K Q F M R Q L S A .

CTGTCCTCAGATGGGGAGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCA
 2701 -----+-----+-----+-----+-----+-----+ 2760
 GACAGGAGTCTACCCCTCCCTGTCCCAGCCGGACATGGGGCCTCCGTGGACCCAGGTAGT
 a L S S D G E G Q G R P V P R R H L G P S .

GAGAAGGTGCAGGTGACAGAGGCGAAGGCAGATGGGGCACTGACCCAGGAGGAGAAAGCA
 2761 -----+-----+-----+-----+-----+-----+ 2820
 CTCTTCACGTCCACTGTCTCCGCTTCCGTCTACCCCGTGACTGGGTCCTCCTCTTTCGT
 a E K V Q V T E A K A D G A L T Q E E K A .

GCCATTGGCACTGTGGAGCTCAGTGTGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGT
 2821 -----+-----+-----+-----+-----+-----+ 2880
 CGGTAACCGTGACACCTCGAGTCACACAAGACCCTAATACGGTTCGGGCACCCCGAGACA
 a A I G T V E L S V F W D Y A K A V G L C .

ACCACGCTGGCCATCTGTCTCCTGTATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAAT
 2881 -----+-----+-----+-----+-----+-----+ 2940
 TGGTGCGACCGGTAGACAGAGGACATACCCAGTTTCACGCCGACGGTAACCTCGGTTA
 a T T L A I C L L Y V G Q S A A A I G A N

GTGTGGCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACACTTCC

Figure 14G

2941 -----+-----+-----+-----+-----+-----+ 3000
CACACCGAGTCACGGACCTGTTTACTACGGTACCGTCTGTCATCTGTCTTGTGTGAAGG

a V W L S A W T N D A M A D S R O N N T S .

CTGAGGCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCA
3001 -----+-----+-----+-----+-----+-----+ 3060
GACTCCGACCCGCAGATACGACGAAATCCTTAAGACGTTCCCAAGAACCACTACGACCGT

a L R L G V Y A A L G I L Q G F L V M L A .

GCCATGGCCATGGCAGCGGGTGGCATCCAGGCTGCCCCTGTGTTGCACCAGGCACTGCTG
3061 -----+-----+-----+-----+-----+-----+ 3120
CGGTACCGGTACCGTCGCCCACCGTAGGTCCGACGGGCACACAACGTGGTCCGTGACGAC

a A M A M A A G G I O A A R V L H Q A L L .

CACAACAAGATACGCTCGCCACAGTCCTTCTTTGACACCACACCATCAGGCCGCATCCTG
3121 -----+-----+-----+-----+-----+-----+ 3180
GTGTTGTTCTATGCGAGCGGTGTCAGGAAGAACTGTGGTGTGGTAGTCCGGCGTAGGAC

a H N K I R S P Q S F F D T T P S G R I L .

AACTGCTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATG
3181 -----+-----+-----+-----+-----+-----+ 3240
TTGACGAAGAGGTTCTGTAGATACAGCAACTACTCCAAGACCGGGGACAGTAGGAGTAC

a N C F S K D I Y V V D E V L A P V I L M .

CTGCTCAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCG
3241 -----+-----+-----+-----+-----+-----+ 3300
GACGAGTTAAGGAAGAAGTTGCGGTAGAGGTGAGAACACCAGTAGTACCGGTCGTGCGGC

a L L N S F F N A I S T L V V I M A S T P .

CTCTTCACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTAT
3301 -----+-----+-----+-----+-----+-----+ 3360
GAGAAGTGACACCAGTAGGACGGGGACCGACACGAGATGTGGAATCACGTCGCGAAGATA

a L F T V V I L P L A V L Y T L V Q R F Y .

GCAGCCACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCC
3361 -----+-----+-----+-----+-----+-----+ 3420

Figure 14H

CGTCGGTGTAGTGCCGTTGACTTCGCCGACCTTAGTCAGTCGGCGAGTGGATAGATGAGG

a A A T S R O L K R L E S V S R S P I Y S .

CACTTTTCGGAGACAGTGACTGGTGCCAGTGTTCATCCGGGCCTACAACCGCAGCCGGGAT
3421 ----- + ----- + ----- + ----- + ----- + ----- + 3480
GTGAAAAGCCTCTGTCACTGACCACGGTCACAGTAGGCCCGGATGTTGGCGTCGGCCCTA

a H F S E T V T G A S V I R A Y N R S R D .

TTTGAGATCATCAGTGATACTAAGGTGGATGCCAACCAGAGAAGCTGCTACCCCTACATC
3481 ----- + ----- + ----- + ----- + ----- + ----- + 3540
AAACTCTAGTAGTCACTATGATTCCACCTACGGTTGGTCTCTTCGACGATGGGGATGTAG

a F E I I S D T K V D A N Q R S C Y P Y I .

ATCTCCAACCGGTGGCTGAGCATCGGAGTGGAGTTCGTGGGGAACTGCGTGGTGCTCTTT
3541 ----- + ----- + ----- + ----- + ----- + ----- + 3600
TAGAGGTTGGCCACCGACTCGTAGCCTCACCTCAAGCACCCCTTGACGCACCACGAGAAA

a I S N R W L S I G V E F V G N C V V L F .

GCTGCACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCT
3601 ----- + ----- + ----- + ----- + ----- + ----- + 3660
CGACGTGATAAACGGCAGTAGCCCTCCTCGTCGGACTTGGGCCCCGACCACCCGGAAAGA

a A A L F A V I G R S S L N P G L V G L S .

GTGTCCTACTCCTTGACAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGAT
3661 ----- + ----- + ----- + ----- + ----- + ----- + 3720
CACAGGATGAGGAACGTCCACTGTAAACGAGACTTGACCTACTATGCTTACTACAGTCTA

a V S Y S L Q V T F A L N W M I R M M S D .

TTGGAATCTAACATCGTGGCTGTGGAGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAG
3721 ----- + ----- + ----- + ----- + ----- + ----- + 3780
AACCTTAGATTGTAGCACCGACACCTCTCCAGTTCTCATGAGGTTCTGTCTCTGTCTC

a L E S N I V A V E R V K E Y S K T E T E .

CGGCCCTGGGTGGTGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCACGTGGGGAGGTG
3781 ----- + ----- + ----- + ----- + ----- + ----- + 3840
CGCGGGACCCACCACCTTCCGTCGGCGGGAGGGCTTCCAACCGGGGGTGCACCCCTCCAC

Figure 14I

a A P W V V E G S R P P E G W P P R G E V .
GAGTTCCGGAATTATTCTGTGCGCTACCGGCCGGCCTAGACCTGGTGCTGAGAGACCTG
3841 -----+-----+-----+-----+-----+-----+ 3900
CTCAAGGCCTTAATAAGACACGCGATGGCCGGCCCGGATCTGGACCACGACTCTCTGGAC

a E F R N Y S V R Y R P G L D L V L R D L .
AGTCTGCATGTCCACGGTGGCGAGAAGGTGGGGATCGTGGGCCGCACTGGGGCTGGCAAG
3901 -----+-----+-----+-----+-----+-----+ 3960
TCAGACGTACACGTGCCACCGCTCTTCCACCCCTAGCACCCGGCGTGACCCCGACCGTTC

a S L H V H G G E K V G I V G R T G A G K .
TCTTCCATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATT
3961 -----+-----+-----+-----+-----+-----+ 4020
AGAAGGTA CTGGGAAACGGACAAGGCGTAGGACCTCCGCCGTTTCCCACTTTAGGCGTAA

a S S M T L C L F R I L E A A K G E I R I .
GATGGCCTCAATGTGGCAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATC
4021 -----+-----+-----+-----+-----+-----+ 4080
CTACCGGAGTTACACCGTCTGTAGCCGGAGGTACTGGACGCGAGAGTCGACTGGTAGTAG

a D G L N V A D I G L H D L R S Q L T I I .
CCGCAGGACCCCATCCTGTTCTCGGGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGC
4081 -----+-----+-----+-----+-----+-----+ 4140
GGCGTCCTGGGGTAGGACAAGAGCCCCTGGGACGCGTACTTGGACCTGGGGAAGCCGTCG

a P Q D P I L F S G T L R M N L D P F G S .
TACTCAGAGGAGGACATTTGGTGGGCTTTGGAGCTGTCCACCTGCACACGTTTGTGAGC
4141 -----+-----+-----+-----+-----+-----+ 4200
ATGAGTCTCCTCCTGTAAACCAACCGAAACCTCGACAGGGTGGACGTGTGCAAACACTCG

a Y S E E D I W W A L E L S H L H T F V S .
TCCAGCCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGC
4201 -----+-----+-----+-----+-----+-----+ 4260
AGGGTCGGCCGTCCGGACCTGAAGGTCACGAGTCTCCCGCCCCTCTTAGAGTCGCACCCG

Figure 14J

a S Q P A G L D F Q C S E G G E N L S V G -
CAGAGGCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTA
4261 ----- + ----- + ----- + ----- + ----- + ----- + 4320
GTCTCCGTCGAGCACACGGACCGGGCTCGGGACGAGGCGTTCTCGGCGTAGGACCAAAAT

a Q R Q L V C L A R A L L R K S R I L V L -
GACGAGGCCACACCTGCCATCGACCTGGAGACTGACAACCTCATCCAGGCTACCATCCGC
4321 ----- + ----- + ----- + ----- + ----- + ----- + 4380
CTGCTCCGGTGTGACGGTAGCTGGACCTCTGACTGTTGGAGTAGGTCCGATGGTAGGCG

a D E A T A A I D L E T D N L I Q A T I R -
ACCCAGTTTGATACCTGCACTGTCCTGACCATCGCACACCGGCTTAACACTATCATGGAC
4381 ----- + ----- + ----- + ----- + ----- + ----- + 4440
TGGGTCAAACATATGGACGTGACAGGACTGGTAGCGTGTGGCCGAATTGTGATAGTACCTG

a T Q F D T C T V L T I A H R L N T I M D -
TACACCAGGGTCCTGGTCCTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAAC
4441 ----- + ----- + ----- + ----- + ----- + ----- + 4500
ATGTGGTCCCAGGACCAGGACCTGTTTCCTCATCATCGACTTAAACTAAGAGGTGCGGTTG

a Y T R V L V L D K G V V A E F D S P A N -
CTCATTGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAA
4501 ----- + ----- + ----- + ----- + ----- + ----- + 4557
GAGTAACGTCGATCTCCGTAGAAGATGCCCTACCGGTCTCTACGACCTGAACGGATT

a L I A A R G I F Y G M A R D A G L A • -

Figure 14K

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MOAT E cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

ATGGCCGCGCCTGCTGAGCCCTGCGCGGGGCAGGGGGTCTGGAACCAGACAGAGCCTGAA
1 -----+-----+-----+-----+-----+-----+ 60
TACCGGCGCGGACGACTCGGGACGCGCCCCGTCCCCCAGACCTTGGTCTGTCTCGGACTT

a M A A P A E P C A G Q G V W N O T E P E -

CCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGGTCTGGGTACCC
61 -----+-----+-----+-----+-----+-----+ 120
GGACGGCGGTGGTCTGGACGACTCGGACACGAAGGACTCTTGTCGTCCCCAGACCCATGGG

a P A A T S L L S L C F L R T A G V W V P -

CCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCCTTTCATCCACCACCATGGCCGG
121 -----+-----+-----+-----+-----+-----+ 180
GGGTACATGGAGACCCAGGAACCAGGGTAGATGGAGGAGAAGTAGGTGGTGGTACCGGCC

a P M Y L W V L G P I Y L L F I H H H G R -

GGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTGCCCCCATA
181 -----+-----+-----+-----+-----+-----+ 240
CCGATGGAGGCCTACAGGGGTGAGAAGTTTCGGTTCTACCACGAACCTAAGCGGGAGTAT

a G Y L R M S P L F K A K M V L G F A L I -

GTCCTGTGTACCTCCAGCGTGGCTGTCGCTCTTTGGAAAATCCAACAGGGAACGCCTGAG
241 -----+-----+-----+-----+-----+-----+ 300
CAGGACACATGGAGGTCGCACCGACAGCGAGAAACCTTTTAGGTTGTCCCTTGCGGACTC

a V L C T S S V A V A L W K I Q Q G T P E -

GCCCCAGAATTCCTCATTCACTACTGTGTGGCTCACCACGATGAGCTTCGCAGTGTTG
301 -----+-----+-----+-----+-----+-----+ 360
CGGGGTCTTAAGGAGTAAGTAGGATGACACACCGAGTGGTGCTACTCGAAGCGTCACAAG

a A P E F L I H P T V W L T T M S F A V F -

CTGATTCACACCGAGAGGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG
361 -----+-----+-----+-----+-----+-----+ 420
GACTAAGTGTGGCTCTCCTTTTCCCTCAGGTCAGTAGACCTCACGACAAACCAATGACC

Figure 15A

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a L I H T E R K K G V Q S S G V L F G Y W .
CTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCAGCAGGCTCCGGAGCGGGCTTC
421 -----+-----+-----+-----+-----+ 480
GAAGAGACGAAACAGAACGGTCGATGGTTGCGACGGGTCGTCCGGAGGCCTCGCCGAAG

a L L C F V L P A T N A A Q Q A S G A G F .
CAGAGCGACCCTGTCCGCCACCTGTCCACCTACCTATGCCTGTCTCTGGTGGTGGCACAG
481 -----+-----+-----+-----+-----+ 540
GTCTCGCTGGGACAGGCGGTGGACAGGTGGATGGATACGGACAGAGACCACCACCGTGTC

a Q S D P V R H L S T Y L C L S L V V A Q .
TTTGTGCTGTCTGCCTGGCGGATCAACCCCCCTTCTCCCTGAAGACCCCAGCAGTCT
541 -----+-----+-----+-----+-----+ 600
AAACACGACAGGACGGACCGCCTAGTTGGGGGGAAGAAGGGACTTCTGGGGGTGTCAGA

a F V L S C L A D Q P P F F P E D P Q Q S .
AACCCCTGTCCAGAGACTGGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT
601 -----+-----+-----+-----+-----+ 660
TTGGGGACAGGTCTCTGACCCCGTCGGAAGGGGAGGTTTCGGTGCAAGACCACCCAAAGA

a N P C P E T G A A F P S K A T F W W V S .
GGCCTGGTCTGGAGGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGGTCGCTTGGG
661 -----+-----+-----+-----+-----+ 720
CCGGACCAGACCTCCCCTATGTCTCCGGTGACTCTGGTTTTCTGGAGACCAGCGAACCC

a G L V W R G Y R R P L R P K D L W S L G .
AGAGAAAACCTCCTCAGAAGAACTTGTTTCCCGGCTTGAAAAGGAGTGGATGAGGAACCGC
721 -----+-----+-----+-----+-----+ 780
TCTCTTTTGAGGAGTCTTCTTGAACAAAGGGCCGAACCTTTTCTCACCTACTCCTTGGCG

a R E N S S E E L V S R L E K E W M R N R .
AGTGCAGCCCGGAGGCACAACAAGGCAATAGCATTTAAAAGGAAAGGCGGCAGTGGCATG
781 -----+-----+-----+-----+-----+ 840
TCACGTCGGGCCTCCGTGTTGTTCCGTTATCGTAAATTTTCTTTCCGCCGTCACCGTAC

Figure 15B

SUBSTITUTE SHEET (RULE 26)

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a S A A R R H N K A I A F K R K G G S G M .
AAGGCTCCAGAGACCGAGCCCTTCCTACGGCAAGAAGGGAGCCAGTGGCGCCCACTGCTG
841 -----+-----+-----+-----+-----+-----+ 900
TTCCGAGGTCTCTGGCTCGGGAAGGATGCCGTTCTCCCTCGGTACCCGCGGGTGACGAC

a K A P E T E P F L R Q E G S Q W R P L L .
AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCCTGGGGACCCTCAGCCTCATCATC
901 -----+-----+-----+-----+-----+-----+ 960
TTCCGGTAGACCGTCCACAAGGTAAGATGGAAGGAGGACCCCTGGGAGTCGGAGTAGTAG

a K A I W Q V F H S T F L L G T L S L I I .
AGTGATGTCTTCAGGTTCACTGTCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGGT
961 -----+-----+-----+-----+-----+-----+ 1020
TCACTACAGAAGTCCAAGTGACAGGGGTTGACGAGTCGGAAAAGGACCTCAAATAACCA

a S D V F R F T V P K L L S L F L E F I G .
GATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCCTCGCCGTGCTGATGTTCTCTCAGCC
1021 -----+-----+-----+-----+-----+-----+ 1080
CTAGGGTTCGGAGGTCGGACCTTCCCGATGGAGGAGCGGCACGACTACAAGGAGAGTCGG

a D P K P P A W K G Y L L A V L M F L S A .
TGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAGG
1081 -----+-----+-----+-----+-----+-----+ 1140
ACGGACGTTTGCGACAACTCGTCGTCTTGACATGTCCGAGTTCACGGCGTCTACTCC

a C L Q T L F E Q Q N M Y R L K V P Q M R .
TTGCGGTGCGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTCC
1141 -----+-----+-----+-----+-----+-----+ 1200
AACGCCAGCCGGTAGTGACCGGACCACATGTCTTCCAGGACCGAGACAGGTGCGCCGAGG

a L R S A I T G L V Y R K V L A L S S G S .
AGAAAGGCCAGTGCGGTGGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCTG
1201 -----+-----+-----+-----+-----+-----+ 1260
TCTTTCGGTCCAGCCACCCACTACACCAGTTAGACCACAGGCACCTGCACGTGCGCCGAC

a R K A S A V G D V V N L V S V D V Q R L .

Figure 15C

WO 99/49735

PCT/US99/06644

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ACCGAGAGCGTCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTGC
 1261 -----+-----+-----+-----+-----+-----+ 1320
 TGGCTCTCGCAGGAGATGGAGTTGCCCACACCGACGGAGAGCAGACCTAGCACAGACG

a T E S V L Y L N G L W L P L V W I V V C -

TTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCCTCACTGCCATCGCTGTCTTCCTG
 1321 -----+-----+-----+-----+-----+-----+ 1380
 AAGCAGATAGAGACCGTCGAGGACCCCGGGAGGCGGGAGTGACGGTAGCGACAGAAGGAC

a F V Y L W Q L L G P S A L T A I A V F L -

AGCCTCCTCCCTCTGAATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGCAA
 1381 -----+-----+-----+-----+-----+-----+ 1440
 TCGGAGGAGGGAGACTTAAAGAAGTAGAGGTTCTTTTCCTTGGTGGTAGTCCTCCTCGTT

a S L L P L N F F I S K K R N H H Q E E Q -

ATGAGGCAGAAGGACTCACGGGCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGACC
 1441 -----+-----+-----+-----+-----+-----+ 1500
 TACTCCGTCTTCCTGAGTGCCCGTGCCGAGTGGTCGAGATAGGAGTCCTTGAGCTTCTGG

a M R Q K D S R A R L T S S I L R N S K T -

ATCAAGTTCCATGGCTGGGAGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCAG
 1501 -----+-----+-----+-----+-----+-----+ 1560
 TAGTTCAAGGTACCGACCCTCCCTCGGAAAGACCTGTCTCAGGACCCGTAGGCTCCGGTC

a I K F H G W E G A F L D R V L G I R G Q -

GAGCTGGGCGCCTTGCGGACCTCCGGCCTCCTCTTCTGTGTGCTGGTGTCTTCCAA
 1561 -----+-----+-----+-----+-----+-----+ 1620
 CTCGACCCGCGGAACGCCTGGAGGCCGGAGGAGAAGAGACACAGCGACCACAGGAAGGTT

a E L G A L R T S G L L F S V S L V S F Q -

GTGTCTACATTTCTGGTCGCACTGGTGGTGGTTTGCTGTCCACACTCTGGTGGCCGAGAAT
 1621 -----+-----+-----+-----+-----+-----+ 1680
 CACAGATGTAAAGACCAGCGTGACCACCACAAACGACAGGTGTGAGACCACCGGCTCTTA

a V S T F L V A L V V F A V H T L V A E N -

Figure 15D

GCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAAGGCC
 1681 -----+-----+-----+-----+-----+-----+ 1740
 CGATACTTACGTCTCTTTTCGGAAACACTGAGAGTGTCAAGAGTTGTAGGAGTTGTTCCGG

a A M N A E K A F V T L T V L N I L N K A .

CAGGCTTTCCTGCCCTTCTCCATCCACTCCCTCGTCCAGGCCCGGGTGTCTTTGACCGT
 1741 -----+-----+-----+-----+-----+-----+ 1800
 GTCCGAAAGGACGGGAAGAGGTAGGTGAGGGAGCAGGTCCGGGCCACAGGAAACTGGCA

a Q A F L P F S I H S L V Q A R V S F D R .

CTGGTCACCTTCTCTGCCTGGAAGAAGTTGACCCTGGTGTCTAGACTCAAGTTCCTCT
 1801 -----+-----+-----+-----+-----+-----+ 1860
 GACCAGTGAAGGAGACGGACCTTCTTCAACTGGGACCACAGCATCTGAGTTCAAGGAGA

a L V T F L C L E E V D P G V V D S S S S .

GGAAGCGCTGCCGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTCCCAG
 1861 -----+-----+-----+-----+-----+-----+ 1920
 CCTTCGCGACGGCCCTTCTAACGTAGTGGTATGTGTACGGTGGAAGCGGACCAGGGTC

a G S A A G K D C I T I H S A T F A W S Q .

GAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCTGGCT
 1921 -----+-----+-----+-----+-----+-----+ 1980
 CTTTCGGGAGGGACGGAGGTGTCTTATTTGGAGTGCCACGGGGTCCCGACAGACGACCGA

a E S P P C L H R I N L T V P Q G C L L A .

GTTGTCCGTCCAGTGGGGGCAGGGAAGTCTCCTGCTGTCCGCCCTCCTTGGGGAGCTG
 1981 -----+-----+-----+-----+-----+-----+ 2040
 CAACAGCCAGGTCACCCCGTCCCTTCAGGAGGGACGACAGGCGGGAGGAACCCCTCGAC

a V V G P V G A G K S S L L S A L L G E L .

TCAAAGGTGGAGGGGTTCTGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGAGGCC
 2041 -----+-----+-----+-----+-----+-----+ 2100
 AGTTTCCACCTCCCCAAGCACTCGTAGCTCCACGACACCGGATGCACGGGGTCTCCGG

a S K V E G F V S I E G A V A Y V P Q E A .

TGGGTGCAGAACACCTCTGTGGTAGAGAATGTGTGCTTCGGGCAGGAGCTGGACCCACCC

Figure 15E

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2101 -----+-----+-----+-----+-----+-----+ 2160
ACCCACGTCTTGTGGAGACACCATCTCTTACACACGAAGCCCGTCCTCGACCTGGGTGGG
a W V Q N T S V V E N V C F G Q E L D P P .
TGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCTGAG
2161 -----+-----+-----+-----+-----+-----+ 2220
ACCGACCTCTCTCATGATCTTCGGACACGGGACGTCGGTCTACACCTGTCTGAAGGGACTC
a W L E R V L E A C A L O P D V D S F P E .
GGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGCAGCGG
2221 -----+-----+-----+-----+-----+-----+ 2280
CCTTAGGTGTGAAGTTAACCCTCGTCCCGTACTTAGAGAGGCCTCCGGTCTTCGTGCGC
a G I H T S I G E O G M N L S G G Q K Q R .
CTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCCCTG
2281 -----+-----+-----+-----+-----+-----+ 2340
GACTCGGACCGGGCCCGACATATGTCTTCCGTGACACATGGACGACCTACTGGGGGAC
a L S L A R A V Y R K A A V Y L L D D P L .
GCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGTGGG
2341 -----+-----+-----+-----+-----+-----+ 2400
CGCCGGGACCTACGGGTGCAACCGGTCGTACAGAAGTTGGTCCAGTAACCCGGACCACCC
a A A L D A H V G Q H V F N Q V I G P G G .
CTACTCCAGGGAACAACACGGATTCTCGTGACGCACGCACTCCACATCCTGCCCCAGGCT
2401 -----+-----+-----+-----+-----+-----+ 2460
GATGAGGTCCCTTGTGTGCCTAAGAGCACTGCGTGCGTGAGGTGTAGGACGGGGTCCGA
a L L Q G T T R I L V T H A L H I L P Q A .
GATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCTACCAGGAGCTT
2461 -----+-----+-----+-----+-----+-----+ 2520
CTAACCTAGTATCACGACCGTTTACCCCGGTAGCGTCTCTACCCAAGGATGGTCCTCGAA
a D W I I V L A N G A I A E M G S Y Q E L .
CTGCAGAGGAAGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA
2521 -----+-----+-----+-----+-----+-----+ 2580

Figure 15F

GACGTCTCCTTCCCCGGGAGCACACAGAAAGACETAGTTCGGTCTGTCCGGTCCTCTATCT

a L Q R K G A L V C L L D Q A R Q P G D R -

GGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCAGAGGCACCTCTGCAGGC
2581 -----+-----+-----+-----+-----+-----+ 2640
CCTCTTCCTCTTTGTCTTGGAACCTGGTCTGGTTCCTGGGGTCTCCGTGGAGACGTCCG

a G E G E T E P G T S T K D P R G T S A G -

AGGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTCCCTGAGAAGGACCGTACC
2641 -----+-----+-----+-----+-----+-----+ 2700
TCCTCCGGGCTCGAATCTGCGCTCTCCAGGTAGTTCAGTCAGGGACTCTTCCTGGCATGG

a R R P E L R R E R S I K S V P E K D R T -

ACTTCAGAAGCCCAGACAGAGGTTCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCA
2701 -----+-----+-----+-----+-----+-----+ 2760
TGAAGTCTTCGGGTCTGTCTCCAAGGAGACCTACTGGGACTGTCCCGTCTACCGGTCTGT

a T S E A Q T E V P L D D P D R A G W P A -

GGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGT
2761 -----+-----+-----+-----+-----+-----+ 2820
CCTTCCTGTCTGTAGGTTATGCCGTCCCACTTCGGGTGTACGTGGACCGGATGGACGCA

a G K D S I Q Y G R V K A T V H L A Y L R -

GCCGTGGGCACCCCCCTCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAGCAAGTGGCC
2821 -----+-----+-----+-----+-----+-----+ 2880
CGGCACCCGTGGGGGGAGACGGAGATGCGTGAGAAGGAGAAGGAGACGGTCGTTACCGG

a A V G T P L C L Y A L F L F L C Q Q V A -

TCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGCGGACGACCCTGCAGTAGGTGGGCAG
2881 -----+-----+-----+-----+-----+-----+ 2940
AGGAAGACGGCCCCGATGACCGACTCGGACACCCGCCTGCTGGGACGTATCCACCCGTC

a S F C R G Y W L S L W A D D P A V G G Q -

CAGACGCAGGCAGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATT
2941 -----+-----+-----+-----+-----+-----+ 3000
GTCTGCGTCCGTCCGGGACGCACCGCCCTAGAAGCCCGAGGAGCCGACAGAGGTTCCGGTAA

Figure 15G

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a Q T Q A A L R G G I F G L L G C L Q A I .
GGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTC
3001 + + + + + 3060
CCCGACAAACGGAGGTACCGACGCCACGAGGATCCACCCGGGCCCCGTAGGTCCAACGAG

a G L F A S M A A V L L G G A R A S R L L .
TTCCAGAGGCTCCTGTGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCC
3061 + + + + + 3120
AAGGTCTCCGAGGACACCCTACACCACGCTAGAGGGTAGTGAAGAACTCGCCTGTGGG

a F Q R L L W D V V R S P I S F F E R T P .
ATTGGTCACCTGCTAAACCGCTTCTCCAAGGAGACAGACACGGTTGACGTGGACATTCCA
3121 + + + + + 3180
TAACCACTGGACGATTTGGCGAAGAGGTTCTCTGTCTGTGCCAACTGCACCTGTAAGGT

a I G H L L N R F S K E T D T V D V D I P .
GACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTG
3181 + + + + + 3240
CTGTTTGAGGGCCAGGGACGACTACATGCGGAAACCTGAGGACCTCCAGTCGGACCACCAC

a D K L R S L L M Y A F G L L E V S L V V .
GCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG
3241 + + + + + 3300
CGTCACCGATGGGGTGACCGGTGACACCGGTAGGACGGTGACAAAGAGGAGATGCGACCC

a A V A T P L A T V A I L P L F L L Y A G .
TTTCAGAGCCTGTATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAGCCAGCTAC
3301 + + + + + 3360
AAAGTCTCGGACATACACCAATCGAGTACGGTCGACTCTGCGAACCTCAGTCGGTCGATG

a F Q S L Y V V S S C Q L R R L E S A S Y .
TCGTCTGTCTGCTCCACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTTC
3361 + + + + + 3420
AGCAGACAGACGAGGGTGTACCGACTCTGCAAGGTCCCGTCGTGTCAACAGGCCCGTAAG

Figure 15H

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a S S V C S H M A E T F Q G S T V V R A F -
CGAACCCAGGCCCTCTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATC
3421 -----+-----+-----+-----+-----+-----+ 3480
GCTTGGGTCCGGGGAGAACACCGAGTCTTGTTACGAGCGCATCTACTTTCGGTCTCCTAG

a R T O A P L V A O N N A R V D E S Q R I -
AGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAAT
3481 -----+-----+-----+-----+-----+-----+ 3540
TCAAAGGGCGCTGACCACCGACTGTCCACCGAACGCCGGTTACACCTCGAGGACCCCTTA

a S F P R L V A D R W L A A N V E L L G N -
GGCCTGGTGTGTTGCAGCTGCCACGTGTGCTGTGCTGAGCAAAGCCACCTCAGTGCTGGC
3541 -----+-----+-----+-----+-----+-----+ 3600
CCGGACCACAAACGTCGACGGTGCACACGACGACTCGTTTCGGGTGGAGTCACGACCG

a G L V F A A A T C A V L S K A H L S A G -
CTCGTGGGCTTCTCTGTCTCTGCTGCCCTCCAGGTGACCCAGGCACTGCAGTGGGTTGTT
3601 -----+-----+-----+-----+-----+-----+ 3660
GAGCACCCGAAGAGACAGAGACGACGGGAGGTCCACTGGGTCCGTGACGTCACCCAACAA

a L V G F S V S A A L Q V T Q A L Q W V V -
CGCAACTGGACAGACCTAGAGAACAGCATCGTGTGCTGAGCGGATGCAGGACTATGCC
3661 -----+-----+-----+-----+-----+-----+ 3720
GCGTTGACCTGTCTGGATCTCTTGTCGTAGCACAGTCACCTCGCCTACGTCCTGATACGG

a R N W T D L E N S I V S V E R M Q D Y A -
TGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCACATGTGCAGCTCAGCCCCCTGGCCT
3721 -----+-----+-----+-----+-----+-----+ 3780
ACCTGCGGGTTCCTCCGAGGGACCTCCGACGGGTGTACACGTCGAGTCGGGGGGACCGGA

a W T P K E A P W R L P T C A A Q P P W P -
CAGGGCGGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATACCGACCTGAGCTCCCGCTG
3781 -----+-----+-----+-----+-----+-----+ 3840
GTCCCGCCCGTCTAGCTCAAGGCCCTGAAACCCGATTCTATGGCTGGACTCGAGGGCGAC

a Q G G Q I E F R D F G L R Y R P E L P L -

Figure 15I

GCTGTGCAGGGCGTGTCCCTCAAGATCCACGCAGGAGAGAAGGTGGGCATCGTTGGCAGG
3841 -----+-----+-----+-----+-----+-----+ 3900
CGACACGTCCCGCACAGGGAGTTCTAGGTGCGTCTCTCTTCCACCCGTAGCAACCGTCC

a A V Q G V S L K I H A G E K V G I V G R -

ACCGGGGCAGGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAG
3901 -----+-----+-----+-----+-----+-----+ 3960
TGGCCCCGTCCCTTCAGGAGGGACCGGTACCCGACGACGCCGAGGTCTCCGTCGACTC

a T G A G K S S L A S G L L R L Q E A A E -

GGTGGGATCTGGATCGACGGGGTCCCCATTGCCACGTGGGGCTGCACACACTGCGCTCC
3961 -----+-----+-----+-----+-----+-----+ 4020
CCACCCTAGACCTAGCTGCCCCAGGGGTAACGGGTGCACCCGACGTGTGTGACGCGAGG

a G G I W I D G V P I A H V G L H T L R S -

AGGATCAGCATCATCCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTC
4021 -----+-----+-----+-----+-----+-----+ 4080
TCCTAGTCGTAGTAGGGGGTCTGGGGTAGGACAAGGGACCGAGAGACGCCTACTTGGAG

a R I S I I P Q D P I L F P G S L R M N L -

GACCTGCTGCAGGAGCACTCGGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTC
4081 -----+-----+-----+-----+-----+-----+ 4140
CTGGACGACGTCTCGTGAGCCTGCTCCGATAGACCCGTGCGGGACCTCTGCCACGTGCGAG

a D L L Q E H S D E A I W A A L E T V Q L -

AAAGCCTTGGTGGCCAGCCTGCCCCGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAG
4141 -----+-----+-----+-----+-----+-----+ 4200
TTTCGGAACCAACCGGTGCGACGGGGCCGGTTCGACGTATGTTACACGACTGGCTCCGCTC

a K A L V A S L P G Q L Q Y K C A D R G E -

GACCTGAGCGTGGGCCAGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC
4201 -----+-----+-----+-----+-----+-----+ 4260
CTGGACTCGCACCCGGTCTTTGTGAGGACACAGACCGTGCACGGGAAGAGGCCTTCTGG

a D L S V G Q K Q L L C I A R A L L R K T -

Figure 15J

CAGATCCTCATCCTGGACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATG
4261 -----+-----+-----+-----+-----+-----+ 4320
GTCTAGGAGTAGGACCTGCTCCGATGACGACGGCACCTGGGACCGTGCCCTCGACGTCTAC

a Q I L I L D E A T A A V D P G T E L O M -

CAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCTCATTGCCACCGCCTG
4321 -----+-----+-----+-----+-----+-----+ 4380
GTCCGGTACGAGCCCTCGACCAAACGTGTACGTGACACGACGAGTAACGGGTGGCGGAC

a Q A M L G S W F A Q C T V L L I A H R L -

CGTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGC
4381 -----+-----+-----+-----+-----+-----+ 4440
GCGAGGCACTACCTGACACGGGCCCCAAGACCAGTACCTGTTCCCCGTCCACCGTCTCTCG

a R S V M D C A R V L V M D K G Q V A E S -

GGCAGCCCGGCCAGCTGCTGGCCCAGAAGGGCCTGTTTTACAGACTGGCCCAGGAGTCA
4441 -----+-----+-----+-----+-----+-----+ 4500
CCGTCGGGCCGGGTGACGACCGGGTCTTCCCGGACAAAATGTCTGACCGGGTCTCAGT

a G S P A Q L L A Q K G L F Y R L A Q E S -

GGCCTGGTCTGA
4501 -----+----- 4512
CCGGACCAGACT

a G L V * -

Figure 15K